

Matches 4: Conservative 13: Mismatches 5: Indels 0: Gaps 0:

Qy 1 XXXXXXXXOQTAPKAPPTXXXXX 22
 Db 9 GTTSSAPSDRAPMAPAMPAGAA 30

Db 4 FMYFVNPASAPKSPAGX 21
 Search completed: February 13, 2001, 12:59:42
 Job time: 114 sec

RESULT 14
 O9TRM4 PRELIMINARY; PRT; 20 AA.

AC O9TRM4
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE 25 KDA PROTEIN P25, PEPTIDE F5A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN 11
 RP SEQUENCE.
 RX MEDLINE=91372400; PubMed=1909972;
 RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
 RA Shirauchi A., Uchida T., Imahori K.;
 RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
 RT Ser/Thr-pro kinase (TPK II) from tau protein kinase fractions.";
 RL FEBS Lett. 289:37-43(1991).
 SO SEQUENCE 20 AA; 2032 MW; 4AADB849A6416897 CRC64;

Query Match 52.5%; Score 32; DB 6; Length 20;
 Best Local Similarity 22.2%; Pred. No. 1e+03;
 Matches 4: Conservative 11: Mismatches 3: Indels 0: Gaps 0:

Qy 6 XXXOQTAPKAPPTXXXXX 23
 Db 1 PANKTPKSPGEPARKDA 18

RESULT 15
 O18764 PRELIMINARY; PRT; 21 AA.
 ID O18764
 AC O18764
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR, BETA 4 SUBUNIT (FRAGMENT).
 GN CHRNA4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98161940; PubMed=9501320;
 RA Tammen I.;
 RT "Genetic mapping of CHRNA3 and CHRNA4 to pig chromosome 7 extends the
 RT syntenic conservation with human chromosome 15 and mouse chromosome
 RT 9.";
 RL Mamm. Genome 9:263-264(1998).
 DR EMBL; AF007797; MNC13376.1; -.
 FT NON_TER 1
 FT NON_TER 21
 SO SEQUENCE 21 AA; 2196 MW; EA98A064013C0FFD CRC64;

Query Match 52.5%; Score 32; DB 6; Length 21;
 Best Local Similarity 27.8%; Pred. No. 1.1e+03;
 Matches 5: Conservative 9: Mismatches 4: Indels 0: Gaps 0:

Qy 1 XXXXXXXXOQTAPKAPPTXX 18
 Db 1 PANKTPKSPGEPARKDA 18


```

09N1U9
ID 09N1U9 PRELIMINARY: PRT: 25 AA.
AC 09N1U9
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE THY-1 T-CELL SURFACE ANTIGEN (FRAGMENT).
GN THY-1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caelano A.R., Shive Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL; AF134236; AAF62349.1; -.
RL NON_TER 1
FT NON_TER 1
SQ SEQUENCE 25 AA: 2674 MW: 0F845E36DFB69A78 CRC64;

```

```

Query Match 54.1%; Score 33; DB 6; Length 25;
Best Local Similarity 14.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 15; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 3 XXXXXXQOTAPKAPPTXXXXXX 23
      : : : : : 1 : : : : :
      1 PVPHTFAVVPQAPSTFGKCKK 21

```

```

RESULT 11
ID 016776 PRELIMINARY: PRT: 27 AA.
AC 016776;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE HISTONE H3 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198991; PubMed=6262733;
RA Clark S.J., Kriegl P.A., Wells J.R.E.;
RT "Isolation of a clone containing human histone genes.";
RL Nucleic Acids Res. 9:1583-1590(1981).
CC -1- FUNCTION: HISTONE H3, ALONG WITH HISTONE H4, PLAYS A CENTRAL ROLE
CC IN NUCLEOSOME FORMATION.
CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATIVELY 146 BP OF DNA.
DR EMBL; V00521; CAA23780.1; -.
DR INTERPRO: IPR000164; -.
DR PROSITE: PS00322; HISTONE_H3_1; UNKNOWN_1.
KW Nuclear protein; Chromosomal protein; DNA-binding; Nucleosome core.
FT NON_TER 27
SQ SEQUENCE 27 AA: 2913 MW: FF25BFAC6A41119B CRC64;

```

```

Query Match 54.1%; Score 33; DB 4; Length 27;
Best Local Similarity 17.4%; Pred. No. 9.9e+02;
Matches 4; Conservative 15; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 1 XXXXXXQOTAPKAPPTXXXXXX 23
      : : : : : 1 : : : : :
      3 RTKOTARKSTGKAPRKQALATKA 25

```

```

RESULT 12
ID 042833 PRELIMINARY: PRT: 29 AA.
AC 042833
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE HISTONE H3 (FRAGMENT).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. STEPTOE;
RX MEDLINE=96188833; PubMed=8628212;
RA Kanazin V., Blake T., Shoemaker R.C.;
RT "Organization of the histone H3 genes in soybean, barley and wheat.";
RL Mol. Gen. Genet. 250:137-147(1996).
CC -1- FUNCTION: HISTONE H3, ALONG WITH HISTONE H4, PLAYS A CENTRAL ROLE
CC IN NUCLEOSOME FORMATION.
CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATIVELY 146 BP OF DNA.
DR EMBL; U38421; AAD09443.1; -.
DR INTERPRO: IPR000164; -.
DR PROSITE: PS00322; HISTONE_H3_1; UNKNOWN_1.
KW Nuclear protein; Chromosomal protein; DNA-binding; Nucleosome core.
FT NON_TER 29
SQ SEQUENCE 29 AA: 3049 MW: 6FCFF25A3D28A41 CRC64;

```

```

Query Match 54.1%; Score 33; DB 10; Length 29;
Best Local Similarity 17.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 15; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 1 XXXXXXQOTAPKAPPTXXXXXX 23
      : : : : : 1 : : : : :
      3 RTKOTARKSTGKAPRKQALATTA 25

```

```

RESULT 13
ID 004024 PRELIMINARY: PRT: 30 AA.
AC 004024;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE NIFB PROTEIN (FRAGMENT).
GN NIFB.
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=384;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PRE;
RX MEDLINE=90136072; PubMed=2693897;
RA Relovink P.M.W., Hontelez J.G.J., Van Kammen A., van den Bos R.C.;
RT "Nucleotide sequence of the regulatory nifA gene of Rhizobium
RT leguminosarum PRE: transcriptional control sites and expression in
RT Escherichia coli.";
RL Mol. Microbiol. 3:1441-1447(1989).
CC -1- FUNCTION: NIFB IS PROBABLY INVOLVED IN THE SYNTHESIS OF THE FE-MO
CC COFACTOR.
CC -1- SIMILARITY: TO OTHER NIFB PROTEINS.
DR EMBL; X17073; CAA34925.1; -.
KW Nitrogen fixation.
FT NON_TER 30
SQ SEQUENCE 30 AA: 3014 MW: 7EC7639389340F5A CRC64;

```

```

Query Match 54.1%; Score 33; DB 2; Length 30;
Best Local Similarity 18.2%; Pred. No. 1.1e+03;

```

OK NCB1_TaxID=881;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=93272123; PubMed=8388770;
 RA Kwoh D.Y., Vedvick T.S., McCue A.F., Gewertz D.;
 RT "Rapid comparison of the cytochrome c3 gene from nine strains of
 RT Desulfovibrio vulgaris using polymerase chain reaction
 RT amplification.";
 RL Can. J. Microbiol. 39:402-411(1993).
 CC -1- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
 CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
 CC DEHYDROGENASE TO FERREDOXIN.
 CC -1- PFM: BINDS FOUR NONPARALLEL HEME GROUPS PER MOLECULE.
 CC HSP: P00132; 2CDV.
 DR HSP: P00132; 2CDV.
 KW Electron transport; sulfate respiration; Heme.
 FT METAL 13 13 IRON (HEME 1 AXIAL LIGAND) (BY
 FT METAL 16 16 SIMILARITY).
 FT METAL 16 16 IRON (HEME 3 AXIAL LIGAND) (BY
 FT NON_TER 23 23 SIMILARITY).
 FT SEQUENCE 23 AA; 2477 MW; 114D6AAC22FAD6B CRC64;

Query Match 55.7%; Score 34; DB 2; Length 23;
 Best Local Similarity 38.5%; Pred. No. 5.9e+02;
 Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY 11 APKAPPTXXXXXX 23
 DB 2 APKAPADGLKMDK 14

RESULT 7
 ID 050180 PRELIMINARY; PRT: 20 AA.
 AC 050180;
 DT 01-JAN-1999 (TREMBlrel. 09, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ACETYL-COENZYME A SYNTHETASE 1 (EC 6.2.1.1) (ACETATE--COA LIGASE 1)
 DE (ACTYL-ACTIVATING ENZYME 1) (FRAGMENT).
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCB1_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PAOI;
 RX MEDLINE=99008987; PubMed=9791103;
 RA Nishijo T., Park S.-M., Lu C.-D., Itoh Y., Abdelal A.T.;
 RT "Molecular characterization and regulation of an operon encoding a
 RT system for transport of arginine and ornithine and the ArgR regulatory
 RT protein in pseudomonas aeruginosa.";
 RL J. Bacteriol. 180:5559-5566(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + ACETATE + COA = AMP + PYROPHOSPHATE +
 CC ACETYL-COA.
 CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
 CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
 DR EMBL; AF012537; AAC71069.1; -.
 DR INTERPRO; IPR000873; -.
 DR PROSITE; PS00455; AMP_BINDING; PARTIAL.
 KW Ligase.
 FT NON_TER 1 1
 FT SEQUENCE 20 AA; 2097 MW; 58E35ED36990522D CRC64;

Query Match 54.1%; Score 33; DB 2; Length 20;
 Best Local Similarity 20.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

OY 3 XXXXXQOTAPKAPPTXXXX 22

DB 1 PRSTPATSPLPTRAWSST 20

RESULT 8
 ID 085736 PRELIMINARY; PRT: 21 AA.
 AC 085736;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
 DE GAGP58 (FRAGMENT).
 OS Murine sarcoma virus.
 OC Viruses; Retroviruses; Retroviridae; Mammalian type C retroviruses.
 OX NCB1_TaxID=11802;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85108156; PubMed=2982040;
 RA Nash M.A., Brizard B.L., Wong J.L., Murphy E.C. Jr.;
 RT "Murine sarcoma virus ts110 RNA transcripts: origin from a single
 RT proviral DNA and sequence of the gag-mos junctions in both the
 RT precursor and spliced viral RNAs.";
 RL J. Virol. 53:624-633(1985).
 DR EMBL; K02857; AAA4657.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 21 AA; 2589 MW; 439B3EB8A51A08PC CRC64;

Query Match 54.1%; Score 33; DB 12; Length 21;
 Best Local Similarity 19.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

OY 3 XXXXXQOTAPKAPPTXXXX 23
 DB 1 REEKERNPKLPWLFITSP 21

RESULT 9
 ID 069350 PRELIMINARY; PRT: 22 AA.
 AC 069350;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE HSV-2 (333) GLYCOPROTEIN C GENE FRAGMENT (0.640 MU) (FRAGMENT).
 OS Herpes simplex virus (type 2).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCB1_TaxID=10310;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85033906; PubMed=6092683;
 RA Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,
 RA Wagner E.K.;
 RT "Herpes simplex virus types 1 and 2 homology in the region between
 RT 0.58 and 0.68 map units.";
 RL J. Virol. 52:615-623(1984).
 DR EMBL; K03358; AAA45838.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 22 AA; 2527 MW; 427404EA94AB3E84 CRC64;

Query Match 54.1%; Score 33; DB 12; Length 22;
 Best Local Similarity 20.0%; Pred. No. 7.9e+02;
 Matches 4; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

OY 1 XXXXXQOTAPKAPPTXXXX 20
 DB 3 VLEHGHSHQPPRRDPTERYV 22

RESULT 10

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 1)
RP
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.
RA Shiraetsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by the
RT Ser/Thr-Pro kinase (PPK II) from tau protein kinase fractions.";
RL *Fers Lett.* 289:37-43(1991).
SQ SEQUENCE 27 AA; 2787 MW; 8DCEFD811407B23 CAC64;

Query Match	60.7%	Score 37	DB 6	Length 27
Best Local Similarity	17.4%	Pred. No.	2.5e+02	
Matches	4	Conservative	16	Mismatches 3
				Indels 0
				Gaps 0

```
Qy 1 XXXXXXXXQGTAPKAPFTXXXXXXXX 23
    ::::: :| |::| :::::
Db 3 DSRPKPANKTPPKSPGEPAKDPA 25
```

RESULT	3			
090UY8				
ID	090UY8	PRELIMINARY:	PRT:	16 AA.
AC	090UY8;			
DT	01-MAY-2000 (TREMBLREL. 13, Created)			
DT	01-MAY-2000 (TREMBLREL. 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLREL. 13, Last annotation update)			
DE	HISTONE H1 (FRAGMENT).			
OS	Cricetulus griseus (Chinese hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Cricetulus.			
OX	NCBI_TaxId=10029;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=66070893; PubMed=7499230;			
RA	Gurley L.R., Valdez J.G., Buchanan J.S.;			
RT	"Characterization of the mitotic specific phosphorylation site of			
RT	histone H1. Absence of a consensus sequence for the p34cdc2/cyclin B			
RT	kinase.".			
RT	J. Biol. Chem. 270:27653-27660(1995).			
RL				
SO	SEQUENCE. 16 AA; 1479 MW; 75ED488737280C8A CRC64;			

Query Match	57.4%	Score 35:	DB 11:	length 16:
Best Local Similarity	33.3%	Pred. No.	2.8e+02:	
Matches	5:	Conservative	2:	Indels 0:
		Mismatches	0:	Gaps 0:

```
QY 9 Q!APKAPTXXXXXXXX 23
    :||| | ::::
Db 2 ETAPAAPAAPAEK 16
```

RESULT	4
091014	
ID	091014
AC	091014
DT	01-OCT-2000 (TREMBlrel. 15, Created)
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE	TAT PROTEIN (FRAGMENT).
CN	TAT.
OS	Human immunodeficiency virus type 1.
OC	Viruses: Retroid viruses; Retroviridae; Lentivirus
OX	NCBI_TaxID=11676:
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=PATIENT 14;

RA Yamada T., Iwamoto A.:
RT "Comparison of proviral accessory genes between long-term
RT nonprogressors and progressors of human immunodeficiency virus type 1
infection."
RT Arch. Virol. 145:1021-1027(2000).
RL EMBL: AB034450; BAA93907.1; -.
DR
FT NON_TER 1 1
SQ SEQUENCE 29 AA; 3064 MW; 937B2E3D51DA719A CRC64;

Query Match	57.4%	Score 35:	DB 12:	length 29:
Best local Similarity	17.4%	Pred. No.	5 3e+02:	
Matches	4:	Conservative	14:	Mismatches 5:
				Indels 0:
				Gaps 0:

```
Qy 1 XXXXXXXXQTAPKAPTXXXXXXX 23
    ::::: | | | :::::
Db 1 PASQPRGDDPTGPKPKKVVETET 23
```

Db 1 PASQPRGDDPTGPKKEPKKVVETET 23

RESULT	5	
P81150		
ID	P81150	PRELIMINARY;
NO	P81150	PRT;
		22 AA

DT	01-JAN-1998	(TREMBLrel, 05, Created)
DT	01-JAN-1998	(TREMBLrel, 05, last sequence update)
DT	01-OCT-2000	(TREMBLrel, 15, last annotation update)

05 Desulfovibrio vulgaris.
0C Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
0X NCBI_TaxID=881;

RP SEQUENCE.
RX MEDLINE=93272123; PubMed=8388770;
RA Kwok D.Y., Vedvick T.S., McCue A.

RT Desulfovibrio vulgaris using polymerase chain reaction
RT amplification.";
RL Can. J. Microbiol. 39:402-411(1993).

CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
CC DEHYDROGENASE TO FERREDOXIN.
CC
CC -I- PTM: BINDS FOUR NONPARALLEL HEME GROUPS PER MOLECULE.

DR	HSSP; P00131; 2CTH.
KW	Electron transport; Sulfate respiration; Heme.
FT	NON_TER 1 1

FT		15	IRON (HEME 3 AXIAL LIGAND) (BY SIMILARITY).
FT	METAL.	15	IRON (HEME 3 AXIAL LIGAND) (BY SIMILARITY).
FT			SIMILARITY).

SEQUENCE 22 AA; 2350 MW; 501C75E1C2225A6C CRC64;

```

Query Match      55.7%:  Score 34:  DB 2:  Length 22:
Best Local Similarity 38.5%:  Pred. NO. 5.6e+02:
Matches      5;  Conservative      7;  Mismatches      1;  Indels      0:  Gaps      0:

```

```
QY      11 APKAPTxxxxxxxx 23
        ||||| :::::
Db      1 APKAPADGLKMEA 13
```

RESULT	6
P81149	
ID	P81149
PRELIMINARY;	
PRT;	23 AA

DT	01-JAN-1998	(TREMBLrel. 05, Created)
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)
DT	01-NOV-1999	(TREMBLrel 12, Last annotation update)

Desulfovibrio vulgaris.
Bacteria; proteobacteria; delta subdivision; Desulfovibrio.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 12:59:40 ; Search time 32.62 Seconds

(without alignments)
82.642 Million cell updates/sec

Title: US-09-372-036-20

Perfect score: 61

Sequence: 1 XXXXXXXXQOTAPKAPTXXXXXX 23

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 10868

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	62.3	27	2	Q9RLM9
2	37	60.7	27	6	Q9LRW3
3	35	57.4	16	11	Q9QUY8
4	35	57.4	29	12	Q9IOI4
5	34	55.7	22	2	P81150
6	34	55.7	23	2	P81149
7	33	54.1	20	2	O50180
8	33	54.1	21	12	O85736
9	33	54.1	22	12	O69350
10	33	54.1	25	6	O9N1U9
11	33	54.1	27	4	O16776
12	33	54.1	29	10	O42833
13	33	54.1	30	2	O04024
14	32	52.5	20	6	O9TRM4
15	32	52.5	21	6	O18764
16	32	52.5	23	2	O9ZG74
17	32	52.5	29	5	O9VMP7
18	32	52.5	29	12	O78846
19	31	50.8	20	8	Q9T218

20	31	50.8	22	5	Q9TW08	Q9TW08 crithidia f
21	31	50.8	24	3	Q07140	Q07140 saccharomyc
22	31	50.8	25	13	O9PSB6	O9PSB6 xenopus lae
23	31	50.8	26	12	O69098	O69098 herpes simp
24	31	50.8	27	2	O9R5D8	O9R5D8 porphyromon
25	31	50.8	28	6	O9XS67	O9XS67 bos taurus
26	31	50.8	28	12	O67786	O67786 human adeno
27	31	50.8	30	4	O9P1D6	O9P1D6 homo sapien
28	30.5	50.0	23	8	O9T2S6	O9T2S6 nicotiana s
29	30	49.2	20	4	O9UC97	O9UC97 homo sapien
30	30	49.2	20	8	O9T219	O9T219 nicotiana s
31	30	49.2	22	8	O9R2H8	O9R2H8 nicotiana s
32	30	49.2	25	2	O9R3H6	O9R3H6 bacillus su
33	30	49.2	27	4	O9UQH1	O9UQH1 homo sapien
34	30	49.2	27	6	O9TR42	O9TR42 bos taurus
35	30	49.2	27	12	O85494	O85494 bovine leuk
36	30	49.2	29	4	O9UKS2	O9UKS2 homo sapien
37	30	49.2	29	4	O9UD94	O9UD94 homo sapien
38	30	49.2	29	12	O73437	O73437 human papil
39	30	49.2	30	4	O9UKS1	O9UKS1 homo sapien
40	30	49.2	30	9	O9T162	O9T162 bacterioph
41	30	49.2	30	11	O9OV42	O9OV42 rattus sp.
42	30	49.2	30	12	O02949	O02949 beet wester
43	29	47.5	20	5	O26805	O26805 trypanosoma
44	29	47.5	20	5	O27385	O27385 trypanosoma
45	29	47.5	22	5	O9TWJ6	O9TWJ6 mytilus edu

ALIGNMENTS

RESULT	ID	Query Match	Score	DB 2:	Length	27:
Q9RLM9	Q9RLM9	PRELIMINARY:	PRT:	27	AA.	
AC	O9RLM9:					
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)					
DE	PORA PROTEIN (FRAGMENT).					
GN	PORA.					
OS	Neisseria meningitidis.					
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.					
OX	NCBI_TaxID=487;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-19/92;					
RA	Wedge E., Gaugant D.A., Musacchio A., Saunders N.B., Zollinger W.D.;					
RT	"Redesignation of a purported PI.15 subtype-specific meningococcal					
RL	monoclonal antibody as a PI.19-specific reagent.";					
DR	EMBL; AJ012728; CAA10151.1; -					
FT	NON_TER					
FT	NON_TER					
SO	SEQUENCE	27	27	2839	MM;	4DAFLFC8585E5FC CRC64;

Query Match 62.3%; Score 38; DB 2: Length 27;
Best local similarity 21.7%; Pred. No. 1.7e+02;
Matches 5; Conservative 14; Mismatches 4; Indels 0; Gaps 0;

Qy 1 XXXXXXXXQOTAPKAPTXXXXXX 23
Db 5 YTPAHFVOOTPSQPTLVPAVVG 27

RESULT 2
Q9TRM3 PRELIMINARY: PRT: 27 AA.
AC Q9TRM3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE 25 KDA PROTEIN P25, PEPTIDE F5B.

Tue Feb 13 16:17:39 2001

Search completed: February 13, 2001, 13:01:15
Job time: 182 sec

us-09-372-036-20.rsp

Matches 4; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 XXXXXXXXQOTAPKAP 15
: : : : : 1 1 1 1
Db 12 SPOOSYLOQPYQNP 26

RESULT 13
CY35_DESAC STANDARD; PRT: 30 AA.

AC P81079;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C3, 50 KDA (FRAGMENT).
OS Desulfuromonas acetoxidans (Chloropseudomonas ethylica).
OC Bacteria; Proteobacteria; delta subdivision; Desulfuromonas group;
CC Desulfuromonas.
RN 111

SEQUENCE.
RX MEDLINE-97419123; PubMed-9271490;
RA Bruschi M., Mondstra M., Guigliarelli B., Asso M., Lojou E.,
Pelliot Y., Abergel C.;
RT "Biochemical and spectroscopic characterization of two new
RT cytochromes isolated from Desulfuromonas acetoxidans.";
RL Biochemistry 36:10601-10608(1997).
CC -1- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
CC DEHYDROGENASE TO FERREDOXIN. THE REDOX POTENTIALS OF THIS
CC CYTOCHROME ARE -140 MV, -210 MV AND -240 MV.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- PTM: BINDS FOUR NONPARALLEL, HEME GROUPS PER MOLECULE.
CC -1- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
DR INTERPRO: IPR000345; -
DR PROSITE: PS00190; CYTOCHROME_C: PARTIAL.
KM Electron transport; Sulfate respiration; Heme; Periplasmic.
FT NON_TER 30
SQ SEQUENCE 30 AA: 3018 MW: B0D52603D5069B8 CRC64;

Query Match 44.3%; Score 27; DB 1; Length 30;
Best Local Similarity 21.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 1 XXXXXXXXQOTAPKAPTXXXXXX 23
: : : : : 1 1 1 1 1 1 1 1
Db 5 VGRDCTIATATGKAKTIAELIIM 27

RESULT 14
TAT_HV12H STANDARD; PRT: 30 AA.

AC P12512;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1 (Zaire H221 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE-89228766; PubMed-2713163;
RA Schulzasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,
McComnick J., Ou C.Y., Myers G., Smith T., Chen E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
RT in 1976: nucleotide sequence of HIV-1 isolated from a serum and
RT generation of hybrid HIV.";
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL: M15896; AAB53949.1; -
DR HIV: M15896; TA952321.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
FT AIDS.
FT NON_TER 1
SQ SEQUENCE 30 AA: 3329 MW: 545F848858040A1F CRC64;

Query Match 44.3%; Score 27; DB 1; Length 30;
Best Local Similarity 13.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 XXXXXXXXQOTAPKAPTXXXXXX 23
: : : : : 1 1 1 1 1 1 1 1
Db 1 PLPTTRGNPTGPKESKESKESKT 23

RESULT 15
FIBB_ANAPL STANDARD; PRT: 18 AA.

AC P12802;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIBRINOPEPTIDE B.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
RN 111

SEQUENCE.
RX MEDLINE-85168193; PubMed-3983613;
RA Min Y., Ping Z., Yaoshi Z.;
RT "Purification and primary structures of duck fibrinopeptides A and
RT B.";
RL Sci. Sin. B. Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR: JP0102; JP0102.
DR INTERPRO: IPR002181; -
DR PROSITE: PS00514; FIBRIN_AG_C:DOMAIN, PARTIAL.
KM Blood coagulation; Plasma; Sulfatation.
FT MOD_RES 1 1
FT MOD_RES 6 6
FT MOD_RES 6 6
FT NON_TER 18
SQ SEQUENCE 18 AA: 2028 MW: B0F15E7768B8A1F9 CRC64;

Query Match 42.6%; Score 26; DB 1; Length 18;
Best Local Similarity 21.4%; Pred. No. 2.1e+03;
Matches 3; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXXXXQOTAPKA 14
: : : : : 1 1 1 1
Db 4 TDYDDESTVPEA 17

DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HISTONE H2B.2, SPERM (FRAGMENT).
 OS Echinus esculentus (sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinzoa;
 CC Echinioidea; Euechinoidea; Echinacea; Echinioidea; Echinidae; Echinus.
 RN 11
 RP SEQUENCE.
 RX MEDLINE=90126812; PubMed=2298202;
 RA Hill C.S., Thomas J.O.;
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal tail of H2B interacts with linker DNA."
 RL Eur. J. Biochem. 187:145-153(1990).
 CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
 DR PIR: S07771; S07771.
 DR INTERPRO: IPR000558; -
 DR PROSITE: PS00357; HISTONE_H2B; PARTIAL.
 KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
 KM Multigene family.
 FT NON_TER
 SQ SEQUENCE 29 AA; 2989 MW; 82EBE7137332E74B CRC64;

Query Match 45.9%; Score 28; DB 1; Length 29;
 Best Local Similarity 25.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 12 PKAPPTXXXXXX 23
 DB 1 PKSPKSPKRG 12

RESULT 10
 ID BRIA_RANES STANDARD; PRT; 24 AA.
 AC P40835;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE BREVININ-1EA.
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 RN 11
 RP SEQUENCE.
 RC TISSUE=SKIN;
 RX MEDLINE=94216303; PubMed=8163497;
 RA Shimaco M., Mignogna G., Barra D., Bossa F.;
 RT "Anticicrobial peptides from skin secretions of Rana esculenta.
 RT Molecular cloning of cDNAs encoding esculentin and brevinins and
 RT Isolation of new active peptides."
 RL J. Biol. Chem. 269:11956-11961(1994).
 CC -1- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST REPRESENTATIVE
 CC GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIAL SPECIES, AND A VERY
 CC HIGH HEMOLYTIC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KW Amphibian skin; Antibiotic; Hemolysis.
 FT DISULFID 18 24 BY SIMILARITY.
 SQ SEQUENCE 24 AA; 2651 MW; 0851EDEDE70F2DFD CRC64;

Query Match 44.3%; Score 27; DB 1; Length 24;
 Best Local Similarity 13.6%; Pred. No. 2.1e+03;
 Matches 3; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

OY 2 XXXXXXQOTAPKAPPTXXXXXX 23
 DB 1 FLPAIFRMAKVPPIICSIK 22

RESULT 11
 ID RL36_DESDE STANDARD; PRT; 26 AA.
 AC Q46501;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L36 (FRAGMENT).
 GN RPMU.
 OS Desulfovibrio desulfuricans.
 CC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=G20;
 RA English R.S., Wall J.D.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U57079; AAB01996.1; -
 DR INTERPRO: IPR000473; -
 DR PFAM: PF00444; Ribosomal_L36; 1.
 DR PROSITE: PS00828; RIBOSOMAL_L36; PARTIAL.
 KW Ribosomal protein.
 FT NON_TER
 SQ SEQUENCE 26 AA; 3022 MW; FB13A4590E5202D4 CRC64;

Query Match 44.3%; Score 27; DB 1; Length 26;
 Best Local Similarity 8.7%; Pred. No. 2.3e+03;
 Matches 2; Conservative 16; Mismatches 5; Indels 0; Gaps 0;

OY 1 XXXXXXQOTAPKAPPTXXXXXX 23
 DB 1 MKVRSYKVKVCPKCKVIRKCVL 23

RESULT 12
 ID HORC_HORSP STANDARD; PRT; 28 AA.
 AC P02864;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE C-HORDEIN (FRAGMENT).
 OS Hordeum spontaneum (Barley).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
 RN 11
 RP SEQUENCE.
 RA Shewry P.R., Autran J.-C., Nimmo C.C., Lew E.J.-L., Kasarda D.D.;
 RT "N-terminal amino acid sequence homology of storage protein components
 RT from barley and a diploid wheat."
 RL Nature 286:520-522(1980).
 CC -1- FUNCTION: SULFUR-POOR SEED STORAGE PROTEIN.
 CC -1- TISSUE SPECIFICITY: DEVELOPING ENDOSPERM.
 DR PIR: A03355; A03355.
 KW Seed storage protein; Multigene family.
 FT NON_TER
 SQ SEQUENCE 28 AA; 3333 MW; 8DBA2DF2494775AA CRC64;

Query Match 44.3%; Score 27; DB 1; Length 28;
 Best Local Similarity 26.7%; Pred. No. 2.5e+03;

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
RN Bovidae; Bovinae; Bos.
RN [1]
RP TISSUE-MILK;
RC MEDLINE-93308294; PubMed-8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
the protease peptone fraction of bovine milk.";
RL J. Dairy Res. 60:189-197(1993).
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KM Glycoprotein; Milk.
FT NON_TER 1 20
GN NON_TER 1
SO SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 49.2%; Score 30; DB 1; Length 20;
Best Local Similarity 25.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

OY 3 XXXXXQOTAPKAPYXXXX 22
DB 1 SXXOPQSONKPLSLK 20

RESULT 7
IPPD_MOUSE STANDARD: PRT: 27 AA.
ID IPPD_MOUSE
AC 060829;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE DOPAMINE- AND CAMP-REGULATED NEURONAL PHOSPHOPROTEIN (DARPP-32)
DE (FRAGMENT).
GN PPPRIB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE-96043524; PubMed-7485543;
RA Blau S., Daly L., Fleenberg A., Teitelman G., Ehrlich M.E.;
RT "DARPP-32 promoter directs transgene expression to renal thick
ascending limb of loop of Henle."
RL Am. J. Physiol. 269:F564-F570(1995).
CC -1- FUNCTION: INHIBITOR OF PROTEIN-PHOSPHATASE 1.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- PTM: DOPAMINE- AND CYCLIC AMP-REGULATED NEURONAL PHOSPHOPROTEIN
(BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PHOSPHATASE INHIBITOR 1 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL: U23160; AAA93223.1;
DR Protein phosphatase inhibitor: Acetylation.
KW MOD_RES 1 ACETYLATION (BY SIMILARITY).
FT NON_TER 1 27
SO SEQUENCE 27 AA; 3139 MW; 2FCB2C85F9458444 CRC64;

Query Match 49.2%; Score 30; DB 1; Length 27;
Best Local Similarity 13.0%; Pred. No. 8.7e+02;

Matches 3; Conservative 16; Mismatches 4; Indels 0; Gaps 0;
OY 1 XXXXXQOTAPKAPYXXXX 23
DB 3 PKDRKKIQFSVPAPSQDLPQV 25

RESULT 8
LIPS_BOVIN STANDARD: PRT: 27 AA.
ID LIPS_BOVIN
AC P16386;
DT 01-AUG-1990 (Rel. 15; Created)
DT 01-AUG-1990 (Rel. 15; Last sequence update)
DT 15-JUL-1998 (Rel. 36; Last annotation update)
DE HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) (FRAGMENT).
KM LIPE.
FT NON_TER 1 27
GN LIPE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
RN Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC MEDLINE-88152238; PubMed-3345839;
RA Garton A.J., Campbell D.G., Cohen P., Yeaman S.J.;
RT "Primary structure of the site on bovine hormone-sensitive lipase
phosphorylated by cyclic AMP-dependent protein kinase.";
RL FEBS Lett. 229:68-72(1988).
RN [2]
RP SEQUENCE OF 8-12, AND PHOSPHORYLATION OF SER-10.
RC TISSUE-ADIPOSE TISSUE;
RX MEDLINE-89137090; PubMed-2537200;
RA Garton A.J., Campbell D.G., Carling D., Hardie D.G., Colbran R.J.,
Yeaman S.J.;
RT "Phosphorylation of bovine hormone-sensitive lipase by the
AMP-activated protein kinase. A possible antilipolytic mechanism.";
RL Eur. J. Biochem. 179:249-254(1989).
CC -1- FUNCTION: IN ADIPOSE TISSUE AND HEART, IT PRIMARILY HYDROLYZES
STORED TRIGLYCERIDES TO FREE FATTY ACIDS, WHILE IN STEROIDGENIC
TISSUES, IT PRINCIPALLY CONVERTS CHOLESTERYL ESTERS TO FREE
CHOLESTEROL FOR STEROID HORMONE PRODUCTION.
CC -1- ENZYME REGULATION: RAPIDLY ACTIVATED BY CAMP-DEPENDENT
PHOSPHORYLATION UNDER THE INFLUENCE OF CATECHOLAMINES.
CC DEPHOSPHORYLATION AND INACTIVATION ARE CONTROLLED BY INSULIN.
CC -1- PATHWAY: HORMONE SENSITIVE LIPASE CATALYZES THE RATE LIMITING
STEP IN TRIGLYCERIDE LIPOLYSIS.
CC -1- SIMILARITY: BELONGS TO THE "GDXG" FAMILY OF LIPOLYTIC ENZYMES.
DR INTERPRO: IPR002168;
DR PROSITE: PS01173; LIPASE_GDXG_HIS; PARTIAL.
DR PROSITE: PS01174; LIPASE_GDXG_SER; PARTIAL.
KW Hydrolase; Lipid degradation; Phosphorylation.
FT NON_TER 1 8
FT MOD_RES 1 8
FT MOD_RES 10 10
FT NON_TER 27 27
SO SEQUENCE 27 AA; 2899 MW; 7ADFA70711D71858 CRC64;

Query Match 45.9%; Score 28; DB 1; Length 27;
Best Local Similarity 13.6%; Pred. No. 1.7e+03;
Matches 3; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

OY 1 XXXXXQOTAPKAPYXXXX 22
DB 6 RRSVSEALITQPEGPLGTSLK 27

RESULT 9
H2B2_ECHES STANDARD: PRT: 29 AA.
AC P13282;
DT 01-JAN-1990 (Rel. 13; Created)
DT 01-FEB-1991 (Rel. 17; Last sequence update)

1

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:01:14 ; Search time 12.53 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-09-372-036-20

Perfect score: 61
Sequence: 1 xxxxxxxxQTAPKAPTXxxxxx 23

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapept 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1785

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	52.5	27	1	PPS1_DROFU
2	31	50.8	25	1	RS20_THERH
3	31	50.8	27	1	LS2_ADE07
4	31	50.8	28	1	G002_TRIMO
5	31	50.8	30	1	ACB1_DIGLA
6	30	49.2	20	1	M117_BOVIN
7	30	49.2	27	1	IPPD_MOUSE
8	28	45.9	27	1	IPPS_BOVIN
9	28	45.9	29	1	H2B2_ECHES
10	27	44.3	24	1	BRI1A_RANES
11	27	44.3	26	1	RL36_DESDE
12	27	44.3	28	1	HORC_HORSP
13	27	44.3	30	1	CY35_DESAC
14	27	44.3	30	1	TAT_HV12H
15	26	42.6	18	1	FTBB_ANAPL
16	26	42.6	19	1	TCBI_TRILO
17	26	42.6	20	1	HELT_HELHO
18	26	42.6	28	1	OST1_CHICK
19	26	42.6	29	1	H0XY_NOCOP
20	26	42.6	29	1	PRO1_DACGL
21	26	42.6	30	1	RNP_ODOVI
22	25	41.0	17	1	RM35_YEAST
23	25	41.0	17	1	TRP2_LEUMA
24	25	41.0	21	1	AROF_STRCO
25	25	41.0	25	1	H2B1_ECHES
26	25	41.0	25	1	PA22_BOYSC
27	25	41.0	26	1	DMS5_PHYBI
28	25	41.0	29	1	DMS5_PHYBI
29	25	41.0	29	1	TAT_HV123
30	24	39.3	12	1	FARI_CALVO
31	24	39.3	17	1	A4SK_MYCBO
32	24	39.3	26	1	RBL_VICFA
33	24	39.3	27	1	DCUP_RHOSH

34	24	39.3	27	1	PHCB_ANANI	P11391 anacyctis n
35	24	39.3	27	1	SODM_DESDE	P11419 desulfovibr
36	24	39.3	28	1	ICPP_VIPLE	P82475 vipera lebe
37	24	39.3	28	1	OMPA_YERPS	P38399 yersinia ps
38	24	39.3	29	1	PSAF_SYNPF	P31083 synechococc
39	24	39.3	30	1	IFRB_RHILE	P80606 rhizobium l
40	24	38.5	19	1	TRP3_LEUMA	P81735 leucophaea
41	23.5	38.5	27	1	NTRC_VITBAL	P19905 vibrilo algi
42	23	37.7	10	1	AL19_CARMA	P81822 carclinus ma
43	23	37.7	13	1	UNO2_PINPS	P81667 pinus pinas
44	23	37.7	14	1	TAT_HV12H	P12509 human immun
45	23	37.7	14	1	TAT_HV12H	P12511 human immun

ALIGNMENTS

```

RESULT 1
ID PPS1_DROFU STANDARD: PRT: 27 AA.
AC P01372:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PARAGONIAL PEPTIDE PS-1 (PARAGONIAL PEPTIDE C).
GN PAPC.
OS Drosophila funebris (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE.
RX MEDLINE=77245908; PubMed=1236144;
RA Baumann H., Wilson K.J., Chen P.S., Hummel R.E.;
RT "The amino-acid sequence of a peptide (PS-1) from Drosophila
RT funebris: a paragonial peptide from males which reduces the
RT receptivity of the female.";
RL Eur. J. Biochem. 52:521-529(1975).
CC -1- FUNCTION: REPRESENTS FEMALE SEXUAL RECEPTIVITY AND STIMULATES
CC OVIPOSITION. THIS PEPTIDE HAS A LOW ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES
CC (PARAGONIAL GLAND).
CC PIR: A01643; PGFPI.
DR EMBLBASE: FBgn0004112; Dfun\Papc.
DR Behavior.
FT VARIANT 2 2 V -> L (IN 30% OF THE MOLECULES).
SQ SEQUENCE 27 AA; 2669 MW; D8083427974AD5D6 CRC64;

Query Match 52.5%; Score 32; DB 1; Length 27;
Best Local Similarity 17.4%; Pred. No. 4.4e+02;
Matches 4; Conservative 15; Mismatches 4; Indels 0; Gaps 0;

OY 1 xxxxxxxxQTAPKAPTXxxxxx 23
DB 5 ANANANNQRTAAKPOANAEASS 27

RESULT 2
ID RS20_THERH STANDARD: PRT: 25 AA.
AC P80382:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S20 (FRAGMENT).
GN RPS2 OR RPS20.
OS Thermus aquaticus (subsp. thermophilus).
OC Bacteria; Thermus/Delinooccus group; Thermus group; Thermus.
RN [1]
RX MEDLINE=95045586; PubMed=7957245;

```


This Page Blank (uspto)

THIS PAGE BLANK (USPTO)

Query Match 57.4% Score 35; DB 2; Length 20;
Best Local Similarity 20.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 13; Mismatches 3; Indels 0; Gaps 0;
OY 4 XXXXXQOTAPKAPKPTXXXXXX 23
Db 1 CLAFHDISPQAPTHFLVIRK 20

RESULT 3
T44453
acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44453
R:Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.
J. Bacteriol. 180, 5559-5566, 1998
A:Title: Molecular characterization and regulation of an operon encoding a system for L-
A:Reference number: 222777; MUID:99008987
A:Accession: T44453
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <NTS>
A:Cross-references: EMBL:AF012537; NID:g2668593; PIDN:AACT1069.1; PID:g2668594
A:Experimental source: strain PA01

Query Match 54.1% Score 33; DB 2; Length 20;
Best Local Similarity 20.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
OY 3 XXXXXQOTAPKAPKPTXXXXXX 22
Db 1 PRSRPSATSPPLPRAMSWT 20

RESULT 4
D53288
major pollen allergen Oue a I - white oak (fragment)
C:Species: Quercus alba (white oak)
C:Date: 02-May-1994 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: D53288
R:Ipsen, H.; Hansen, O.C.
Mol. Immunol. 28, 1279-1288, 1991
A:Title: The NH2-terminal amino acid sequence of the immunochemically partial identical
s) Car b I and oak (Quercus alba) Oue a I pollens.
A:Reference number: A53288; MUID:92072607
A:Accession: D53288
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-24 <IP>
A:Cross-references: PID:g239736; PIDN:AA20454.1
A:Experimental source: pollen
A:Note: Sequence extracted from NCBI backbone (NCBIP:68410)
C:Superfamily: pathogenesis-related protein
C:Keywords: pollen

Query Match 54.1% Score 33; DB 2; Length 24;
Best Local Similarity 26.1%; Pred. No. 7.9e+02;
Matches 6; Conservative 14; Mismatches 3; Indels 0; Gaps 0;
OY 1 XXXXXQOTAPKAPKPTXXXXXX 23
Db 1 GVFTXESQETSVIAPALFKALF 23

RESULT 5
137460
histone H3 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999

C:Accession: I37460
R:Clark, S.J.; Krieg, P.A.; Wells, J.R.
Nucleic Acids Res. 9, 1583-1590, 1981
A:Title: Isolation of a clone containing human histone genes.
A:Reference number: I37460; MUID:81198991

A:Accession: I37460
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-27 <RES>
A:Cross-references: EMBL:V00521; NID:g32094; PIDN:CAA23780.1; PID:g32095
C:Superfamily: histone H3

Query Match 54.1% Score 33; DB 2; Length 27;
Best Local Similarity 17.4%; Pred. No. 8.9e+02;
Matches 4; Conservative 15; Mismatches 4; Indels 0; Gaps 0;

OY 1 XXXXXQOTAPKAPKPTXXXXXX 23
Db 3 RTKOTARKSTGKAPRKOLATKA 25

RESULT 6
E26627
apolipoprotein C-II - crab-eating macaque (fragment)
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 31-Dec-1993
C:Accession: E26627
R:Herbert, P.N.; Bausserman, L.L.; Lynch, K.M.; Saritelli, A.L.; Kantor, M.A.; Nicolo
Biochemistry 26, 1457-1463, 1987
A:Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (
A:Reference number: A26627; MUID:87185451
A:Accession: E26627
A:Molecule type: protein
A:Residues: 1-27 <HEK>
C:Superfamily: apolipoprotein A-I
C:Keywords: chylomicron; lipid binding; lipoprotein; VLDL

Query Match 54.1% Score 33; DB 2; Length 27;
Best Local Similarity 20.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

OY 4 XXXXXQOTAPKAPKPTXXXXXX 23
Db 1 AQOPQODEPSPALISOVQE 20

RESULT 7
T04412
histone H3 - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T04412
R:Kanazin, V.; Blake, T.; Shoemaker, R.C.
Mol. Gen. Genet. 250, 137-147, 1996
A:Title: Organization of the histone H3 genes in soybean, barley and wheat.
A:Reference number: Z15345; MUID:96188833
A:Accession: T04412
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-29 <KAN>
A:Cross-references: EMBL:U38421; NID:g1053054; PIDN:AAD09443.1; PID:g1053055
A:Experimental source: cv. Streptoc

C:Genetics:
A:Map position: 4
A:Introns: 24/3
C:Superfamily: histone H3
C:Keywords: chromosomal protein; DNA binding; nucleosome core

Query Match 54.1% Score 33; DB 2; Length 29;
Best Local Similarity 17.4%; Pred. No. 9.6e+02;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 12:59:05 ; Search time 20.45 Seconds
(without alignments)

76.367 Million cell updates/sec

Title: US-09-372-036-20

Perfect score: 61
Sequence: 1 XXXXXXXXXQTPAKAPTXXXXXX 23

Scoring table: BLUSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 6242

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.4	20	2	A33878	myosin light chain
2	57.4	20	2	S72501	protein kinase C i
3	54.1	20	2	T44453	acetyl-CoA synthet
4	54.1	24	2	D53288	major pollen aller
5	54.1	27	2	I37460	histone H3 - human
6	54.1	27	2	E26627	apolipoprotein C-I
7	54.1	29	2	T04412	histone H3 - barle
8	54.1	30	2	S06966	hypothetical prote
9	52.5	26	2	D32248	Ig kappa chain V r
10	52.5	27	1	PCFF1	paragonial peptide
11	52.5	29	2	T35132	hypothetical prote
12	50.8	20	2	P00687	photosystem I 14.1
13	50.8	22	2	D47256	photosystem I 19.3
14	50.8	24	2	S13656	matrix protein - h
15	50.8	25	2	S51071	ribosomal protein
16	50.8	27	2	A49236	fibroblast-activat
17	50.8	28	2	A03356	omega-gliadin - ei
18	50.0	23	2	A48186	ATP synthase beta-
19	49.2	20	2	P00688	photosystem I 14.0
20	49.2	22	2	P00667	photosystem I 19.3
21	49.2	24	2	I54329	gene NF1 protein -
22	49.2	27	2	A48988	chitinase (EC 3.2.
23	47.5	16	2	S03405	hydrogenase (EC 1.
24	47.5	20	2	S68619	histone H3 - sea u
25	47.5	27	2	B43853	probable phosphogl
26	47.5	29	2	S57225	labial protein (cl
27	47.5	30	2	D72276	hypothetical prote
28	45.9	13	2	A60458	protocatechuate 3,
29	45.9	22	2	S58433	isocitrate dehydro

30	45.9	22	2	I41299	T-cell receptor be
31	45.9	24	2	S70329	omega 1-40 secalin
32	45.9	24	2	PC2001	major allergen - E
33	45.9	24	2	I38253	T-cell acute lymph
34	45.9	25	2	S52124	alpha-gliadin S11
35	45.9	25	2	I40692	cema protein (Iga1
36	45.9	27	2	S00347	triacylglycerol 11
37	45.9	28	2	S56121	ICL6 protein - Par
38	45.9	28	2	F46522	T-cell receptor et
39	45.9	28	2	C61233	conceptus protein
40	45.9	29	2	S07771	histone H2B.2, spe
41	45.9	29	2	S11613	ribosomal protein
42	45.9	30	2	I52394	fibronectin, splic
43	45.1	28	2	S11129	phosphoprotein, bo
44	44.3	14	2	S11129	flagellar motor sw
45	44.3	20	2	PS0028	

ALIGNMENTS

RESULT 1
A33878
Myosin light chain kinase, smooth muscle - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 07-Nov-1997
C:Accession: A33878
J. Ikebe, M. Maruta, S. J. Beardon, S. R. Biol. Chem. 264, 6867-6971, 1989
A:Title: Location of the inhibitory region of smooth muscle myosin light chain kinase
A:Reference number: A33878; MUID:89214114
A:Accession: A33878
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <IKK>
C:Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homo
C:Keywords: smooth muscle

Query Match 57.4%; Score 35; DB 2; Length 20;
Best Local Similarity 25.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
QY 4 XXXXQOTAPKAPTXXXXXX 23
DB 1 KKPAKTPKAPTPQITQF 20

RESULT 2
S72501
protein kinase C inhibitor - human (fragment)
N:Alternate names: histidine triad nucleotide-binding protein
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S72501; S62623
R:Maines, M.D.; Trakshel, G.M.
Arch. Biochem. Biophys. 300, 320-326, 1993
A:Title: Purification and characterization of human biliverdin reductase.
A:Reference number: S29736; MUID:93143333
A:Accession: S72501
A:Molecule type: protein
A:Residues: 1-20 <MAI>
A>Note: this protein was identified as biliverdin reductase; the identification is qu
R:Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Eur. J. Biochem. 235, 372-381, 1996
A:Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati
A:Reference number: S62622; MUID:96202961
A:Accession: S62623
A:Molecule type: protein
A:Residues: 1-20 <MAV>
C:Superfamily: protein kinase C inhibitor; histidine triad homology
C:Keywords: homodimer; protein kinase inhibitor; zinc

This Page Blank (uspto)

THIS PAGE BLANK (USPTO)

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-412-227C-29

Query Match 80.3% Score 49; DB 8; Length 11;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 XQOTAPKAPTX 17
:|||||:
Db 1 QOQTAPKAPTE 11

RESULT 15
US-09-372-036-29

Sequence 29, Application US/09372036
GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUHRT, ANDREAS
APPLICANT: COEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372.036

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/456,670

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/075,248

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4239567.4

FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4219111.4

FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1694D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

TELEX: 64191

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-09-372-036-29

Query Match 80.3% Score 49; DB 17; Length 11;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 XQOTAPKAPTX 17
:|||||:
Db 1 QOQTAPKAPTE 11

Search completed: February 13, 2001, 13:00:58
Job time: 189 sec

TELEFAX: 703-243-6410
TELE: 64191
INFORMATION FOR SEQ. ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: *Listeria monocytogenes*
STRAIN: EGD
US-08-412-227-29

Query Match	80.3%	Score 49	DB 8	Length 11
Best Local Similarity	81.8%	Pred. No. 4.1		
Matches 9	Conservative	2	Mismatches 0	Indels 0
			Gaps 0	

```
OY 7 XQQTAPKAPT'X 17
      :|||||:
Db 1 QQQTAPKAPTE 11
```

RESULT 13
US-08-412-227A-29

GENERAL INFORMATION:
APPLICANT: SCHOUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWELLER, WINFRIED
APPLICANT: BÜRGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US-08/412,227A

```

```

: APPLICATION NUMBER: US 08/075,248
: FILING DATE: 11-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4239567.4
: FILING DATE: 25-NOV-1992
: PRIOR APPLICATION DATA:
:
:

```

; INFORMATION FOR SEQ ID NO: 29:

```

? SEQUENCE CHARACTERISTICS:
? LENGTH: 11 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? ORIGINAL SOURCE:
? ORGANISM: Listeria monocytogenes
? STRAIN: EGD
? OS-08-412-227A-29

```

Query Match	80.3%	Score 49	DB 8	Length 11
Best Local Similarity	81.8%	Pred. No.	4.1	
Matches	9	Conservative	2	Mismatches 0
				Indels 0
				Gaps 0

```
QY      7 XQQTAPKAPTX 17
          :|||||||:
Db      1 QOQTAPKAPTE 11
```

US-08-412-227C-29
: Sequence 29, Application US/08412227C

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/412,227C

```

```

: FILING DATE: 11-JUN-1993
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4239567.4
: FILING DATE: 25-NOV-1992
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4219111.4

```

TELEX: 64191

```

LENGTH: 11 amino acids
TYPE: amino acid

```

FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-412-227C-42

Query Match 82.0%; Score 50; DB 8; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 XXOOTAPKAPTX 17
DB 1 CQOOTAPKAPTE 12

RESULT 11
US-09-372-036-42
Sequence 42, Application US/09372036
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372.036
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/456,670
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4

FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-372-036-42

Query Match 82.0%; Score 50; DB 17; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 XXOOTAPKAPTX 17
DB 1 CQOOTAPKAPTE 12

RESULT 12
US-08-412-227-29
Sequence 29, Application US/08412227
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412.227
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1502
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,227
FILING DATE: 25-NOV-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1502
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-412-227-42

Query Match 82.0%; Score 50; DB 8; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 XXQQTAPKAPTX 17
:|||||
DB 1 CQQTAPKAPTE 12

RESULT 9
US-08-412-227A-42
Sequence 42, Application US/08412227A
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWELLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MULLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,227A
FILING DATE: 27-MAR-1995

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-412-227A-42

Query Match 82.0%; Score 50; DB 8; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 XXQQTAPKAPTX 17
:|||||
DB 1 CQQTAPKAPTE 12

RESULT 10
US-08-412-227C-42
Sequence 42, Application US/08412227C
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWELLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MULLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,227C
FILING DATE: 27-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4

Best Local Similarity 42.9%; Pred. No. 0.44;
Matches 9; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

OY 1 XXXXXXXXOQTAPKAPTXXXX 21
Db 1 KKETATOOQTAPKAPTEAKP 21

RESULT 6

US-08-988-444-33
Sequence 33, Application US/08988444
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988.444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-988-444-33

Query Match 96.7%; Score 59; DB 13; Length 21;
Best Local Similarity 42.9%; Pred. No. 0.44;

Matches 9; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

OY 1 XXXXXXXXOQTAPKAPTXXXX 21
Db 1 KKETATOOQTAPKAPTEAKP 21

RESULT 7

US-09-217-849-33
Sequence 33, Application US/09217849
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR

TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-217-849-33

Query Match 96.7%; Score 59; DB 16; Length 21;
Best Local Similarity 42.9%; Pred. No. 0.44;
Matches 9; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

OY 1 XXXXXXXXOQTAPKAPTXXXX 21
Db 1 KKETATOOQTAPKAPTEAKP 21

RESULT 8

US-08-412-227-42
Sequence 42, Application US/08412227
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, Siegfried
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOEBEL, ANDREAS
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412.227C
FILING DATE: 27-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
NAME/KEY: Modified-site
LOCATION: 17-23
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-412-227C-20

Query Match 100.0%; Score 61; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 xxxxxxxxOQTAPKAPTxxxxxx 23
Db 1 xxxxxxxxOQTAPKAPTxxxxxx 23

RESULT 2
US-09-372-036-20
Sequence 20, Application US/09372036
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFFERD
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF INVENTION: 43
CORRESPONDENCE ADDRESSES:
ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA

COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372.036
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/456,670
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
NAME/KEY: Modified-site
LOCATION: 17-23
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-09-372-036-20

Query Match 100.0%; Score 61; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 xxxxxxxxOQTAPKAPTxxxxxx 23
Db 1 xxxxxxxxOQTAPKAPTxxxxxx 23

RESULT 3
US-08-479-520-33
Sequence 33, Application US/08479520
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF INVENTION: 40
CORRESPONDENCE ADDRESSES:

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:00:57 ; Search time 73.72 Seconds
(without alignments)
47.213 Million cell updates/sec

Title: US-09-372-036-20
Perfect score: 61
Sequence: 1 xxxxxxxxQQTAPKAPRxxxxxxx 23

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 928122 seqs, 151327723 residues

Total number of hits satisfying chosen parameters: 290408

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents-AA:*
1: /cgn2_6/ptodata/2/paa/PCUUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/2/paa/US103_COMB.pep.*
28: /cgn2_6/ptodata/2/paa/US104_COMB.pep.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	23	8	US-08-412-227C-20
2	61	100.0	23	17	US-09-372-036-20
3	59	96.7	21	8	US-08-479-520-33
4	59	96.7	21	8	US-08-486-050-33
5	59	96.7	21	8	US-08-486-050A-33

6	59	96.7	21	13	US-08-988-444-33	Sequence 33, Appl
7	59	96.7	21	16	US-09-217-849-33	Sequence 33, Appl
8	50	82.0	12	8	US-08-412-227-42	Sequence 42, Appl
9	50	82.0	12	8	US-08-412-227A-42	Sequence 42, Appl
10	50	82.0	12	8	US-08-412-227C-42	Sequence 42, Appl
11	50	82.0	12	17	US-09-372-036-42	Sequence 42, Appl
12	49	80.3	11	8	US-08-412-227-29	Sequence 29, Appl
13	49	80.3	11	8	US-08-412-227A-29	Sequence 29, Appl
14	49	80.3	11	8	US-08-412-227C-29	Sequence 29, Appl
15	49	80.3	11	17	US-09-372-036-29	Sequence 29, Appl
16	47	77.0	9	8	US-08-412-227-20	Sequence 20, Appl
17	47	77.0	9	8	US-08-412-227A-20	Sequence 20, Appl
18	46	75.4	25	1	PCR-US000-09215-1	Sequence 1, Appl1
19	46	75.4	25	19	US-09-544-793-1	Sequence 1, Appl1
20	46	75.4	25	22	US-60-128-500-1	Sequence 1, Appl1
21	40	65.6	21	3	US-07-949-836-72	Sequence 72, Appl
22	40	65.6	21	3	US-07-949-836C-72	Sequence 72, Appl
23	38	62.3	21	13	US-08-989-477-7	Sequence 7, Appl1
24	38	62.3	21	13	US-08-989-477-7	Sequence 7, Appl1
25	38	62.3	30	1	PCR-US98-21346-3	Sequence 3, Appl1
26	38	62.3	30	13	US-08-948-131-3	Sequence 3, Appl1
27	37	60.7	11	8	US-08-412-227-38	Sequence 38, Appl
28	37	60.7	11	8	US-08-412-227A-38	Sequence 38, Appl
29	37	60.7	11	8	US-08-412-227C-38	Sequence 38, Appl
30	37	60.7	11	17	US-09-372-036-38	Sequence 38, Appl
31	37	60.7	24	16	US-09-270-767-61651	Sequence 61651, A
32	37	60.7	26	22	US-60-236-359-20812	Sequence 20812, A
33	37	60.7	28	22	US-60-173-464-5237	Sequence 5237, Ap
34	36	59.0	28	3	US-07-663-442-84	Sequence 84, Appl
35	35	57.4	7	8	US-08-479-520-34	Sequence 34, Appl
36	35	57.4	7	8	US-08-486-050-34	Sequence 34, Appl
37	35	57.4	7	8	US-08-486-050A-34	Sequence 34, Appl
38	35	57.4	7	13	US-08-988-444-34	Sequence 34, Appl
39	35	57.4	7	13	US-08-988-444-34	Sequence 34, Appl
40	35	57.4	9	8	US-08-217-849-34	Sequence 25, Appl
41	35	57.4	9	8	US-08-412-227-25	Sequence 25, Appl
42	35	57.4	9	8	US-08-412-227A-25	Sequence 25, Appl
43	35	57.4	9	8	US-08-412-227C-25	Sequence 25, Appl
44	35	57.4	9	17	US-09-372-036-25	Sequence 25, Appl
45	35	57.4	17	19	US-09-547-596-97	Sequence 97, Appl
			17	19	US-09-547-735-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-412-227C-20
Sequence 20, Application US/08412227C
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-34

Query Match 57.4%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OOTAPKA 14
111111
Db 1 OOTAPKA 7

RESULT 12
US-08-482-847-34
Sequence 34, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: SHAMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-34

Query Match 57.4%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 OOTAPKA 14
111111
Db 1 OOTAPKA 7

RESULT 13
US-08-456-670B-25
Sequence 25, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD

FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria innocua
US-08-456-670B-38

Query Match 60.7%; Score 37; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 XOOTAPKAPTQ 17
:|||||
DB 1 EOOTTTKAPTQ 11

RESULT 9
US-09-136-251-5
Sequence 5, Application US/09136251A
Patent No. 6127156
GENERAL INFORMATION:
APPLICANT: HOSHINO, Tatsuo
APPLICANT: MIYAZAKI, Taro
APPLICANT: OJIMA, Setsuko
APPLICANT: SHINDOH, Masako
APPLICANT: TOMIYAMA, No. 61271561bun1
TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
FILE REFERENCE: D-Sorbitol Dehydrogenase Gene
CURRENT APPLICATION NUMBER: US/09136,251A
CURRENT FILING DATE: 1998-08-19
EARLIER APPLICATION NUMBER: EP 97114432.4
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 24
TYPE: PRT
ORGANISM: Gluconobacter suboxydans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (22)
US-09-136-251-5

Query Match 60.7%; Score 37; DB 3; Length 24;
Best Local Similarity 27.3%; Pred. No. 56;
Matches 6; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

QY 1 XXXXXXXXOOTAPKAPTQXXXXX 22
:|||||
DB 3 QSYFAGPSQYAPQAPGVNAXNL 24

RESULT 10

US-08-920-610-10
Sequence 10, Application US/08920610
Patent No. 6015709
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS, AND
TITLE OF INVENTION: COMPOSITIONS AND USES RELATED THERETO
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,610
FILING DATE: 27-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-006.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-920-610-10

Query Match 59.0%; Score 36; DB 3; Length 26;
Best Local Similarity 17.4%; Pred. No. 88;
Matches 4; Conservative 15; Mismatches 4; Indels 0; Gaps 0;

QY 1 XXXXXXXXOOTAPKAPTQXXXXX 23
:|||||
DB 3 LALAPAPQVLPQAPAPAPAPAM 25

RESULT 11
US-08-127-499A-34
Sequence 34, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNASSAY FOR
DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3820
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-72

Query Match      65.6%; Score 40; DB 2; Length 21;
Best Local Similarity 23.8%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXXXXQOTAPKAPTXXXX 21
Db 1 YSOAITCCKTAPOKPKEDPFK 21

RESULT 7
US-08-726-306A-171
Sequence 171, Application US/08/726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
```

```
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-171

Query Match      62.3%; Score 38; DB 2; Length 24;
Best Local Similarity 25.0%; Pred. No. 40;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 XXXXXXXXQOTAPKAPTXXXX 20
Db 5 PRPASVAVQAPPOAFTWTR 24

RESULT 8
US-08-456-670B-38
Sequence 38, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HOFMANN, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
```

APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-456-670B-42

Query Match 82.0%; Score 50; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 0.27;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 XXQQTAPKAPTX 17
Db 1 QOOTAPKAPTE 12

RESULT 5
US-08-456-670B-29
; Sequence 29, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA

APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-29

Query Match 80.3%; Score 49; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.33;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 XXQQTAPKAPTX 17
Db 1 QOOTAPKAPTE 11

RESULT 6
US-08-934-915-72
; Sequence 72, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 17-23
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-20

Query Match 100.0%; Score 61; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 XXXXXXXQQTAPKAPTYXXXXX 23
Db 1 XXXXXXXQQTAPKAPTYXXXXX 23

RESULT 2
US-08-127-499A-33
Sequence 33; Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-33

Query Match 96.7%; Score 59; DB 1; Length 21;
Best Local Similarity 42.9%; Pred. No. 0.031;
Matches 9; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

OY 1 XXXXXXXQQTAPKAPTYXXXX 21
Db 1 KKETATQQTAPKAPTEAKP 21

RESULT 3
US-08-482-847-33
Sequence 33; Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-33

Query Match 96.7%; Score 59; DB 1; Length 21;
Best Local Similarity 42.9%; Pred. No. 0.031;
Matches 9; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

OY 1 XXXXXXXQQTAPKAPTYXXXX 21
Db 1 KKETATQQTAPKAPTEAKP 21

RESULT 4
US-08-456-670B-42
Sequence 42; Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK protein - protein search, using sw model

Run on: February 13, 2001, 12:58:10 ; Search time 19.09 Seconds
(without alignments)
21.635 Million cell updates/sec

Title: US-09-372-036-20

Perfect score: 61
Sequence: 1 XXXXXXXXQOTAPKAPTXXXXXX 23

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 111283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	23	2	US-08-456-670B-20
2	59	96.7	21	1	US-08-127-499A-33
3	59	96.7	21	1	US-08-482-847-33
4	50	82.0	12	2	US-08-456-670B-42
5	49	80.3	11	2	US-08-456-670B-29
6	40	65.6	21	2	US-08-934-915-72
7	38	62.3	24	2	US-08-726-306A-171
8	37	60.7	11	2	US-08-456-670B-38
9	37	60.7	24	3	US-09-136-251-5
10	36	59.0	26	3	US-08-920-610-10
11	35	57.4	7	1	US-08-127-499A-34
12	35	57.4	7	1	US-08-482-847-34
13	35	57.4	9	2	US-08-456-670B-25
14	35	57.4	29	1	US-08-367-198A-2
15	34.5	56.6	25	2	US-08-473-475A-12
16	34	55.7	21	1	US-08-127-499A-24
17	34	55.7	21	1	US-08-482-847-24
18	34	55.7	25	1	US-07-976-358-21
19	34	55.7	26	2	US-08-894-339-6
20	33	54.1	13	2	US-08-456-670B-36
21	33	54.1	15	2	US-08-560-558E-2
22	33	54.1	21	5	5204326-22
23	33	54.1	22	2	US-04-481-793-36
24	33	54.1	22	2	US-08-354-326-36
25	33	54.1	22	4	PCT-US95-07068-36
26	33	54.1	24	1	US-07-976-358-24
27	33	54.1	24	1	US-08-205-938A-41
28	33	54.1	24	1	US-07-794-288D-190

29	33	54.1	24	4	PCT-US95-02626-41	Sequence 41, Appl
30	33	54.1	25	1	US-07-976-358-15	Sequence 15, Appl
31	33	54.1	25	1	US-07-794-288D-182	Sequence 182, Appl
32	33	54.1	25	2	US-08-456-670B-23	Sequence 23, Appl
33	33	54.1	26	1	US-08-450-360-11	Sequence 11, Appl
34	33	54.1	28	1	US-07-596-081A-14	Sequence 14, Appl
35	33	54.1	29	5	5204326-118	Patent No. 5204326
36	33	54.1	30	1	US-08-205-938A-40	Sequence 40, Appl
37	33	54.1	30	1	US-08-121-054C-20	Sequence 20, Appl
38	33	54.1	30	1	US-08-121-054C-21	Sequence 21, Appl
39	33	54.1	30	1	US-08-121-054C-22	Sequence 22, Appl
40	33	54.1	30	1	US-08-121-054C-26	Sequence 26, Appl
41	33	54.1	30	1	US-08-121-054C-27	Sequence 27, Appl
42	33	54.1	30	1	US-08-121-054C-28	Sequence 28, Appl
43	33	54.1	30	2	US-08-934-915-190	Sequence 190, Appl
44	33	54.1	30	2	US-08-934-915-193	Sequence 193, Appl
45	33	54.1	30	3	US-07-401-432-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-456-670B-20
Sequence 20, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWELLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

XX Claim 35: Page 77: 98pp: English.
 PS
 CC R73913 is the *Listeria monocytogenes* protein P60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in R73891-R73894 and R73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 XX
 SQ Sequence 7 AA:

Query Match 57.4%; Score 35; DB 16; length 7;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QQTAPKA 14
 |||||
 Db 1 qqtapka 7

Search completed: February 13, 2001, 12:58:41
 Job time: 56 sec

```

PF 06-JUL-1993; 93WO-FR00695.
XX
PR 08-JUL-1992; 92FR-0008429.
PA (RHON ) RHONE POULENC RORER SA.
PI
XX Bolotin M, Menart S;
XX
DR WPI: 1994-035074/04.
DR N-PSDB: Q54886.
XX
PT New transcriptional promoter from kluyveromyces lactis ribosome
PT protein gene - provides efficient expression of heterologous
PT proteins, esp. human serum albumin, in yeasts without glucose
PT repression
XX
PS Disclosure; Page 16; 28pp; Franch.
XX
CC The promoter of the Kluyveromyces lactis rp28 ribosome protein gene
CC provides highly efficient expression of heterologous proteins in
CC Kluyveromyces (or other hosts) e.g. enzymes, blood components,
CC insulin, lymphokines, growth factors, apolipoproteins, antigens for
CC vaccine production or fusion proteins. Since the promoter is not
CC repressed by glucose it can be used with standard culture media.
XX
SQ Sequence 30 AA:
XX
Query Match 59.0%; Score 36; DB 15; Length 30;
Best Local Similarity 21.7%; Pred. NO. 2.5e+02;
Matches 5; Conservative 15; Mismatches 3; Indels 0; Gaps 0
QY 1 XXXXXXXXQQTAPKAPTXXXXXX 23
Db :::::||||: :::::|
8 kghkrshnrtaqskdnylklilx 30
XX
RESULT 15
R73906 R73906 standard; peptide; 7 AA.
XX
AC R73906;
XX
DT 05-DEC-1995 (first entry)
XX
DE Listeria monocytogenes protein p60 precursor peptide 292-298.
XX
KW Listeria monocytogenes; protein p60 precursor; vaccine;
KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
KW immunosassay; diagnosis; treatment; prophylactic; bacterial;
KW viral; peptide 292-298.
XX
OS Listeria monocytogenes.
XX
PN WO9509232-A.
XX
PD 06-APR-1995.
XX
PE 28-SEP-1994; 94WO-CA00516.
XX
PR 28-SEP-1993; 93US-0127499.
XX
PA (SHAR/) SHARMA L R.
PA (VALS/) VAN ALSTYNE D.
XX
PI Sharma LR, Van Alstyne D;
XX
DR WPI: 1995-147431/19.
XX
PT New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis

```



```

XX DE Listeria p60 peptide-epitope.
XX XX Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX KW Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX FT Region 1..7
XX FT /note= "opt. 0-7 amino acid residues"
XX FT 17..23
XX FT /note= "opt. 0-7 amino acid residues"
XX FT
XX PN DE4318450-A.
XX PD 16-DEC-1993.
XX PE 03-JUN-1993; 93DE-4318450.
XX PR 11-JUN-1992; 92DE-4219111.
XX PR 25-NOV-1992; 92DE-4239567.
XX PA (MERCK ) MERCK PATENT GMBH.
XX PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
XX PI Hofmann G, Buber A, Goebel W, Koehler S;
XX DR WPI; 1993-406956/51.
XX PT New primers for PCR detection of Listeria - including individual
XX PT species, also new peptide(s) for raising antibodies for
XX PT immunochemical detection
XX PS
XX PS Claim 3; Page 4; 19pp; German.
XX CC The sequence is that of a Listeria p60 peptide epitope which
XX CC which may be used in the prodn. of antibodies for the detection
XX CC of Listeria by immunoassay (partic. ELISA). It may be used as
XX CC part of a method that allows determination of individual Listeria
XX CC species, esp. L. monocytogenes.
XX CC
XX SO Sequence 23 AA:

Query Match 80.3%; Score 49; DB 14; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXXQOTAPKAPTXXXXXX 23
   ||||||||| |||||||||
Db 1 xxxxxxxxqgttkaptxxxxxx 23

RESULT 5
R54618
ID R54618 standard; Protein: 9 AA.
XX
AC R54618;
XX
DT 16-JUN-1994 (first entry)
XX
DE Listeria p60 peptide epitope.
XX
KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX OS Synthetic.
XX PN DE4318450-A.
XX PD 16-DEC-1993.
XX PE 03-JUN-1993; 93DE-4318450.
XX

```

```

PR 11-JUN-1992; 92DE-4219111.
PR 25-NOV-1992; 92DE-4239567.
XX
XX PA (MERCK ) MERCK PATENT GMBH.
XX PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
XX PI Hofmann G, Buber A, Goebel W, Koehler S;
XX DR WPI; 1993-406956/51.
XX PT New primers for PCR detection of Listeria - including individual
XX PT species, also new peptide(s) for raising antibodies for
XX PT immunochemical detection
XX PS
XX PS Disclosure; Page 3; 19pp; German.
XX CC The sequence is that of a Listeria p60 peptide epitope which
XX CC which may be used in the prodn. of antibodies for the detection
XX CC of Listeria by immunoassay (partic. ELISA). It may be used as
XX CC part of a method that allows determination of individual Listeria
XX CC species, esp. L. monocytogenes.
XX CC
XX SO Sequence 9 AA;

Query Match 77.0%; Score 47; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QOTAPKAPT 16
   |||||||||
Db 1 qgttkapt 9

RESULT 6
R15594
ID R15594 standard; Protein: 21 AA.
XX
AC R15594;
XX
DT 02-MAR-1992 (first entry)
XX
DE Immunopeptide derived from HPV31 L1 peptide.
XX
KW cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
XX KW squamous cell carcinoma; ELISA; HPV 31.
XX
XX OS Synthetic.
XX OS WO9118294-A.
XX PN 28-NOV-1991.
XX PD
XX PF 13-MAY-1991; 91WO-SE00335.
XX PR 11-MAY-1990; 90SE-0001705.
XX PA (MEDS-) MEDSCAND AB.
XX PI Dillner J, Dillner L, Cheng HM;
XX DR WPI; 1991-369390/50.
XX PT Diagnosis of human papilloma virus infection and PV-carrying
XX PT tumours - using synthetic peptide(s) to detect virus specific
XX PT antigen-antibody complexes by immunoassay
XX PS
XX PS Disclosure; Page 39; 72pp; English.
XX CC This is one of a large number of peptides which have been
XX CC synthesised on the basis of the amino acid sequences for the E2, E4,
XX CC E7, L1 or L2 proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The
XX CC selection of peptide sequences was based on the assumption that an

```

XX	New primers for PCR detection of <i>Listeria</i> - including individual
PT	species, also new peptide(s) for raising antibodies for
PT	Immunochemical detection
XX	
PS	Claim 3; Page 4; 19pp; German.
XX	
CC	The sequence is that of a <i>Listeria</i> p60 peptide epitope which
CC	which may be used in the prodn. of antibodies for the detection
CC	of <i>Listeria</i> by Immunoassay (partic. ELISA). It may be used as
CC	part of a method that allows determination of individual <i>Listeria</i>
CC	species, esp. <i>L. monocytogenes</i> .
XX	
SO	Sequence 23 AA:
XX	
QY	1 xxxxxxxxOOTAAPKAPTXxxxxxx 23
Db	1 xxxxxxxxqtapkaplxxxxxx 23
XX	
RESULT	2
R73894	
XX	R73894 standard; peptide; 21 AA.
AC	
XX	R73894:
DT	
XX	05-DEC-1995 (first entry)
DE	
XX	<i>Listeria</i> monocytogenes protein p60 precursor peptide 285-305.
KW	<i>Listeria</i> monocytogenes; protein p60 precursor; vaccine;
KW	meningitis related homologous antigenic sequence; MRHNS; RV-1;
KW	immunassay; diagnosis; treatment; prophylactic; bacterial;
XX	viral; peptide 285-305.
XX	
OS	<i>Listeria</i> monocytogenes.
XX	
PN	WO9509232-A.
XX	
PD	06-APR-1995.
XX	
PF	28-SEP-1994; 94WO-CA00516.
XX	
PR	28-SEP-1993; 93US-0127499.
XX	
PA	(SHAR/) SHARMA L R.
PA	(VALS/) VAN ALSTYNE D.
XX	
PI	Sharma LR, Van Alstyne D;
XX	
DR	WPI: 1995-147431/19.
XX	
PT	New peptide(s) and corresp. antibodies for the treatment of
PT	meningitis - the peptide(s) corresp. to homologous antigenic
PT	sites on bacterial and viral agents and on chemokine(s), used for
PT	detecting and preventing meningitis
XX	
PS	Claim 34; Page 74; 98pp; English.
XX	
CC	R73913 is the <i>Listeria</i> monocytogenes protein p60 precursor. It
CC	contains the meningitis related antigenic sequences (MRHNS) claimed
CC	in R73891-R73894 and R73903-R73906, which are recognised by a
CC	monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
CC	claimed MRHNS peptides may be used in immunoassays to diagnose the
CC	presence of bacterial and/or viral meningitis agents in a sample,
CC	or in prophylactic and therapeutic meningitis treatments. The
CC	peptides may also be used as vaccines against meningitis.
XX	

```

SO      Sequence      21 AA:

Query Match
Best Local Similarity      96.7%; Score 59; DB 16; Length 21;
Matches      9; Conservative      12; Mismatches      0; Indels      0; Gaps      0;

QY      1 XXXXXXXXOQTAPKAPTXXXXX 21
        ::::|||||:::
Db       1 kketatgqtapkapteaakp 21

RESULT      3
R45171
ID      R45171 standard; Protein; 11 AA.
XX
AC      R45171;
XX
DT      16-JUN-1994 (first entry)
XX
DE      Listeria p60 peptide epitope.
XX
KW      Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX
OS      Synthetic.
XX
PN      DE4318450-A.
XX
PD      16-DEC-1993.
XX
PF      03-JUN-1993; 93DE-4318450.
XX
PR      11-JUN-1992; 92DE-4219111.
XX
PR      25-NOV-1992; 92DE-4239567.
XX
PA      (MERE ) MERCK PATENT GMBH.
PI      Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
PI      Hofmann G, Buberl A, Goebel W, Koehler S;
XX
DR      WPI; 1993-406956/51.
XX
PT      New primers for PCR detection of Listeria - including individual
PT      species, also new peptide(s) for raising antibodies for
PT      immunochemical detection
XX
PS      Disclosure; Fig 2; 19pp; German.
XX
CC      The sequence is that of a Listeria p60 peptide epitope which
CC      which may be used in the prodn. of antibodies for the detection
CC      of Listeria by immunoassay (partic. ELISA). It may be used as
CC      part of a method that allows determination of individual Listeria
CC      species, esp. L. monocytogenes.
XX
SQ      Sequence      11 AA:

Query Match
Best Local Similarity      80.3%; Score 49; DB 14; Length 11;
Matches      9; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      7 XQQTAPKAPTXX 17
        :|||||:
Db       1 qqtapkapte 11

RESULT      4
R45167
ID      R45167 standard; Protein; 23 AA.
XX
AC      R45167;
XX
DT      16-JUN-1994 (first entry)

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 12:58:39 ; Search time 25.91 Seconds

(without alignments)
30.353 Million cell updates/sec

Title: US-09-372-036-20

Perfect score: 61
Sequence: 1 XXXXXXXOCTAPKAPYXXXXXX 23

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 151408

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_36:*

1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT:*

9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT:*

10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	23	14	R45162
2	59	96.7	21	16	R73894
3	49	80.3	11	14	R45171
4	49	80.3	23	14	R45167
5	47	77.0	9	14	R54618
6	40	65.6	21	12	R15594
7	38	62.3	20	21	Y81345
8	38	62.3	24	19	Y20846
9	38	62.3	30	20	Y09351
10	37	60.7	11	14	R54627
11	37	60.7	24	20	W95022
12	36	59.0	26	20	Y03840

13	36	59.0	28	13	R27561	Insert A to prevent
14	36	59.0	30	15	R47193	N-terminal fragment
15	35	57.4	7	16	R73906	Listeria monocytog
16	35	57.4	9	14	R54623	Listeria p60 pepti
17	35	57.4	20	17	W16969	NCK SH3 domain-bin
18	35	57.4	20	18	W25344	NCK SH3 domain-bin
19	35	57.4	25	13	R23617	V3 peptide A - abl
20	35	57.4	30	20	Y36687	Fragment of human
21	34.5	56.6	25	19	W10257	Hepatitis GB virus
22	34	55.7	19	18	W65668	Fibronectin bindin
23	34	55.7	21	16	R73890	Streptococcus pneu
24	34	55.7	24	14	R44646	Calcitonin fragmen
25	34	55.7	24	14	R44647	Calcitonin fragmen
26	34	55.7	25	15	R53665	HDAG' domain #7 of
27	34	55.7	26	17	W03573	Compacting oligope
28	34	55.7	28	19	W83961	Polypeptide encode
29	33	54.1	13	14	R54625	Listeria innocua p
30	33	54.1	15	17	R96287	Light chain fragmen
31	33	54.1	20	19	W17132	Rabbit 3-phosphoin
32	33	54.1	21	14	R11959	Fragment of squamo
33	33	54.1	24	14	R44642	Calcitonin fragmen
34	33	54.1	24	14	R44643	Calcitonin fragmen
35	33	54.1	24	15	R53668	HDAG' antigen HR-2
36	33	54.1	24	16	R83677	Insect antiBacteri
37	33	54.1	24	17	R87649	Synthetic Bordetel
38	33	54.1	24	17	Y25653	Quercus alba aller
39	33	54.1	25	14	R45165	Listeria p60 pepti
40	33	54.1	25	15	R53659	HDAG' domain #1 of
41	33	54.1	25	15	V51254	Monoclonal antibod
42	33	54.1	26	14	R32370	NP-2. Homo sapien
43	33	54.1	28	12	R13378	Adult T-cell leuka
44	33	54.1	28	20	Y41484	Fragment of human
45	33	54.1	30	9	P82664	1,7-alpha-L-amino

ALIGNMENTS

RESULT 1	
ID R45162	standard: protein: 23 AA.
AC R45162	
XX	
DT 16-JUN-1994	(first entry)
XX	
DE	Listeria p60 peptide epitope.
XX	
KW	Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Region
FT	Region
FT	Region
FT	Region
XX	
PN	DE4318450-A.
XX	
PD	16-DEC-1993.
XX	
PF	03-JUN-1993; 93DE-4318450.
XX	
PR	11-JUN-1992; 92DE-4219111.
PR	25-NOV-1992; 92DE-4239567.
XX	
PA	(MERCK) MERCK PATENT GMBH.
XX	
PI	Schubert P, Neumann S, Pawelzik W, Linxweiler W, Burger C;
PI	Hofmann G, Bubert A, Goedel W, Koehler S;
XX	
DR	WPI: 1993-406956/51.

This Page Blank (uspt~)


```
RESULT 11
ID 079913 PRELIMINARY; PRT; 27 AA.
AC 079913;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE NMDII DEHYDROGENASE SUBUNIT 1 (FRAGMENT).
GN NDI.
OS Leiopeltis belliana.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Leiopeltinae;
OC Leiopeltis.
OX NCBI_TaxID=52196;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97315309; PubMed=9169559;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the
RT mitochondrial genome among Iguanian lizards."
RL J. Mol. Evol. 44:660-674(1997).
DR EMBL; U82689; AAC62285.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 27 AA; 2923 MW; 48692549309ECFEE CRC64;

Query Match 67.4%; Score 31; DB 8; Length 27;
Best Local Similarity 15.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXXXPVAPTOXXXXXX 20
Db 7 LHMCLVITAPALASLPN 26

RESULT 12
ID 059396 PRELIMINARY; PRT; 29 AA.
AC 059396;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE NADPH-CYTOCHROME C REDUCTASE (EC 1.8.1.2) (SULFITE REDUCTASE (NADPH)
DE (FRAGMENT)).
DR Eukaryota; Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93083978; PubMed=1452024;
RA Loudon J.A., Loughlin R.E.;
RT "Mutagenesis and regulation of the cysJ promoter of Escherichia coli
RT K-12."
RL Gene 122:17-25(1992).
CC -1- CATALYTIC ACTIVITY: H(2)S + 3 NADP(+) + 3 H(2)O -> SULFITE + 3
CC NADPH.
CC -1- COFACTOR: FAD; FMN; HEME.
DR EMBL; M65058; AAA23649.1; -.
KW Oxidoreductase; NADP.
FT NON_TER
SQ SEQUENCE 29 AA; 3092 MW; 3F5CC6AACCA3091A CRC64;

Query Match 67.4%; Score 31; DB 2; Length 29;
Best Local Similarity 15.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 XXXXXXXPVAPTOXXXXXX 20
Db 5 VPSALLPLNPEQLARLQAA 24

RESULT 13
ID 004024 PRELIMINARY; PRT; 30 AA.
AC 004024;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE NIFB PROTEIN (FRAGMENT).
GN NIFB.
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=384;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PRE;
RX MEDLINE=90136072; PubMed=2693897;
RA Rosivink P.M.W., Hontela J.G.J., Van Kamen A., van den Bos R.C.;
RT "Nucleotide sequence of the regulatory nifA gene of Rhizobium
RT leguminosarum PRE: transcriptional control sites and expression in
RT Escherichia coli."
RL Mol. Microbiol. 3:1441-1447(1989).
CC -1- FUNCTION: NIFB IS PROBABLY INVOLVED IN THE SYNTHESIS OF THE FE-MO
CC COFACTOR.
CC -1- SIMILARITY: TO OTHER NIFB PROTEINS.
CC EMBL; X17073; CAA34925.1; -.
DR NITROGEN fixation.
FT NON_TER
SQ SEQUENCE 30 AA; 3014 MW; 7EC7639389340F5A CRC64;
```

```
Query Match 67.4%; Score 31; DB 2; Length 30;
Best Local Similarity 16.7%; Pred. No. 1.7e+03;
Matches 3; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXXXPVAPTOXXXXXX 18
Db 13 SAPSDRAPMAPMGAA 30

RESULT 14
ID 090V14 PRELIMINARY; PRT; 30 AA.
AC 090V14;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE COLLAGENASE INHIBITOR MS-22 (FRAGMENT).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105266; PubMed=7806596;
RA Rosenchal R.A., Moses M.A., Shintani Y., Megyesi J.F., Langer R.,
RA Folkman J.;
RT "Purification and characterization of two collagenase inhibitors from
RT mouse sarcoma 180 conditioned medium."
RL J. Cell. Biochem. 56:97-105(1994).
DR HSSP; P16035; 1BR9.
DR INTERPRO; IPR001820; -.
DR PROSITE; PS00288; TIMP; 1.
SQ SEQUENCE 30 AA; 3232 MW; EB658F1186284D9 CRC64;

Query Match 67.4%; Score 31; DB 11; Length 30;
Best Local Similarity 23.5%; Pred. No. 1.7e+03;
```

Query Match 67.4%; Score 31; DB 4; Length 14;

Db 4 PGEVYDDPIDPVEPEPELKT 23

```
GN 7AT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 17;
RA Yamada T., Iwamoto A.;
RT "Comparison of proviral accessory genes between long-term
RT nonprogressors and progressors of human immunodeficiency virus type 1
RT infection.";
RL Arch. Virol. 145:1021-1027(2000).
DR EMBL; AB034454; BAA93911.1; -.
FT NON_TER
FT 1
SQ SEQUENCE 29 AA; 3085 MW; 83CF9F3D51DA7255 CRC64;

Query Match 76.1%; Score 35; DB 12; Length 29;
Best Local Similarity 15.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXXPVAPTOXXXXXX 20
Db 2 ASOPRGDPGPTESKKVES 21

RESULT 3
O9P1D6 PRELIMINARY; PRT; 30 AA.
AC O9P1D6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PR02366 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,
RA Liu M., He F.;
RT "Functional prediction of the coding sequences of 121 new genes
RT deduced by analysis of cDNA clones from human fetal liver.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF116700; AAF71120.1; -.
FT NON_TER
FT 1
SQ SEQUENCE 30 AA; 3095 MW; B867AC02CAE6054A CRC64;

Query Match 73.9%; Score 34; DB 4; Length 30;
Best Local Similarity 20.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXXPVAPTOXXXXXX 20
Db 6 LPTPRLAPASTQSVCEVT 25

RESULT 4
O9I156 PRELIMINARY; PRT; 27 AA.
AC O9I156;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS POL.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_Taxid=11103;
RN [1]
SQ SEQUENCE
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 9 LBI;
RA Izopet J., Rostang L., Sandres K., Cisterne J.M., Pasquier C.,
RA Rumeau J.L., Duffaut M., Durand D., Puel J.;
RT "Longitudinal analysis of Hepatitis C virus replication and liver
RT fibrosis progression in renal transplant recipients.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207208; AAF75414.1; -.
FT NON_TER
FT 1
SQ SEQUENCE 27 AA; 2738 MW; 21A99879DEE3D687 CRC64;

Query Match 71.7%; Score 33; DB 12; Length 27;
Best Local Similarity 15.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXXPVAPTOXXXXXX 20
Db 3 VVNGGRRIAPAGLVSLFNP 22

RESULT 5
O84069 PRELIMINARY; PRT; 29 AA.
AC O84069;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE INFLUENZA A/BELAMV/42 (H1N1), NON-STRUCTURAL PROTEIN
DE (SEG 8), COOH TERMINUS OF NS1 (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
OX NCBI_Taxid=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "Nonsense mutations affecting the lengths of the NS1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00956; AAA43517.1; -.
DR INTERPRO; IPR000256; -.
DR PFM; PF00600; Flu_NS1; 1.
FT NON_TER
FT 1
SQ SEQUENCE 29 AA; 3395 MW; A6A6A4710F3FEBB CRC64;

Query Match 71.7%; Score 33; DB 12; Length 29;
Best Local Similarity 15.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXXPVAPTOXXXXXX 20
Db 5 SNENGRPLTPKOKKRMART 24

RESULT 6
O9UC97 PRELIMINARY; PRT; 20 AA.
AC O9UC97;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE RAS-RELATED SMALL GTPASE 5A (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
SQ SEQUENCE
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 12:57:48 : Search time 32.62 Seconds
(without alignments)
71.863 Million cell updates/sec

Title: US-09-372-036-17
Perfect score: 46
Sequence: 1 XXXXXXXPVAPPTQXXXXXX 20

Scoring table:
BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 10868

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-REMBL.15.*
2: SP-archaea.*
3: SP-bacteria.*
4: SP-fungi.*
5: SP-human.*
6: SP-invertebrate.*
7: SP-mammal.*
8: SP-mhc.*
9: SP-organelle.*
10: SP-phage.*
11: SP-plant.*
12: SP-rodent.*
13: SP-virus.*
14: SP-vertebrate.*
15: SP-unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	35	76.1	29	12	Q910I1	Q910I1 human immun
2	35	76.1	29	12	Q910I0	Q910I0 human immun
3	34	73.9	30	4	Q9P1D6	Q9P1D6 homo sapien
4	33	71.7	27	12	Q91L56	Q91L56 hepatitis c
5	33	71.7	29	12	Q84069	Q84069 influenza a
6	32	69.6	20	4	Q9UC97	Q9UC97 homo sapien
7	32	69.6	27	13	Q57545	Q57545 lampetra pl
8	31	67.4	14	4	Q9UC10	Q9UC10 homo sapien
9	31	67.4	23	12	Q65291	Q65291 human adeno
10	31	67.4	23	12	Q9QSP0	Q9QSP0 human adeno
11	31	67.4	27	8	Q79913	Q79913 leishmania b
12	31	67.4	29	2	Q59396	Q59396 escherichia
13	31	67.4	30	2	Q04024	Q04024 rhizobium l
14	31	67.4	30	11	Q9QV14	Q9QV14 mus sp. col
15	30	65.2	19	12	Q84862	Q84862 human saplen
16	30	65.2	22	4	Q9NS53	Q9NS53 homo sapien
17	30	65.2	25	6	Q9N1U9	Q9N1U9 equus caball
18	30	65.2	28	12	Q9QD27	Q9QD27 rabies viru
19	30	65.2	28	12	Q9QD26	Q9QD26 rabies viru

20	30	65.2	28	12	Q9QD25	Q9QD25 rabies viru
21	30	65.2	28	12	Q9QD24	Q9QD24 rabies viru
22	30	65.2	28	12	Q9QD23	Q9QD23 rabies viru
23	30	65.2	28	12	Q9QD22	Q9QD22 rabies viru
24	30	65.2	28	12	Q9QD21	Q9QD21 rabies viru
25	30	65.2	28	12	Q9QD20	Q9QD20 rabies viru
26	30	65.2	28	12	Q9QD19	Q9QD19 rabies viru
27	30	65.2	28	12	Q9QD18	Q9QD18 rabies viru
28	30	65.2	28	12	Q9QD17	Q9QD17 rabies viru
29	30	65.2	28	12	Q9QD16	Q9QD16 rabies viru
30	30	65.2	28	12	Q9QD15	Q9QD15 rabies viru
31	30	65.2	28	12	Q9QD14	Q9QD14 rabies viru
32	30	65.2	28	12	Q9QD13	Q9QD13 rabies viru
33	30	65.2	28	12	Q9QD12	Q9QD12 rabies viru
34	30	65.2	28	12	Q9QD11	Q9QD11 rabies viru
35	30	65.2	28	12	Q9QD10	Q9QD10 rabies viru
36	30	65.2	28	12	Q9QD09	Q9QD09 rabies viru
37	30	65.2	28	12	Q9QD08	Q9QD08 rabies viru
38	30	65.2	28	12	Q9QD07	Q9QD07 rabies viru
39	30	65.2	28	12	Q9QD06	Q9QD06 rabies viru
40	30	65.2	29	3	Q01370	Q01370 neurospora
41	30	65.2	29	4	Q9UKS2	Q9UKS2 homo sapien
42	30	65.2	29	4	Q9UD94	Q9UD94 homo sapien
43	30	65.2	30	3	Q9UR69	Q9UR69 trameces ve
44	30	65.2	30	6	Q9TTE7	Q9TTE7 atetes belz
45	29	63.0	18	4	Q9NSF0	Q9NSF0 homo sapien

ALIGNMENTS

RESULT 1
ID Q910I1 PRELIMINARY: PRT: 29 AA.
AC Q910I1:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE TAT PROTEIN (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 17;
RA Yamada T., Iwamoto A.;
RT "Comparison of proviral accessory genes between long-term
nonprogressors and progressors of human immunodeficiency virus type 1
infection.";
RL Arch. Virol. 145:1021-1027(2000).
DR EMBL: AB034453; BAA3910.1; -
FT NON-TER 1 1
SQ SEQUENCE 29 AA; 3013 MW; 83CFCF3D51DA7255 CRC64;

Query Match 76.1%; Score 35; DB 12; Length 29;
Best Local Similarity 15.0%; Pred. NO. 3.6e+02;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXXXPVAPPTQXXXXXX 20
DB 2 ASQPRDPTGPTESKKYVES 21
RESULT 2
ID Q910I0 PRELIMINARY: PRT: 29 AA.
AC Q910I0:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE TAT PROTEIN (FRAGMENT).

This Page Blank (uspto)

THIS PAGE BLANK (USPTO)

```

KW Membrane.
FT MOD_RES 1 1 ACETYLACTION. (TO FORM AIB).
FT MOD_RES 1 1 METHYLATION (TO FORM AIB).
FT MOD_RES 4 4 METHYLATION (TO FORM AIB).
FT MOD_RES 5 5 METHYLATION (TO FORM AIB).
FT MOD_RES 7 7 METHYLATION (TO FORM AIB).
FT MOD_RES 8 8 METHYLATION (TO FORM AIB).
FT MOD_RES 9 9 METHYLATION (TO FORM AIB).
FT MOD_RES 12 12 METHYLATION (TO FORM AIB).
FT MOD_RES 15 15 METHYLATION (TO FORM AIB).
FT MOD_RES 16 16 METHYLATION (TO FORM AIB).
FT MOD_RES 16 16 METHYLATION (TO FORM AIB).
FT MOD_RES 19 19 ETHYLATION (TO FORM IVA, IN BII).
SO SEQUENCE 19 AA; 1756 MW; B908C2DEFF883D38 CRC64;

QY 1 XXXXXXVPAPTOX 14
   : : : : : | | | :
Db 6 QAAASLAPVAAQOL 19

RESULT 13
FEDB_AMYME STANDARD; PRT; 21 AA.
ID FEDB_AMYME P80706;
AC P80706;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE FORMATE ESTER DEHYDROGENASE, BETA CHAIN (EC 1.2.99.-) (FEDB)
DE (FRAGMENT).
OS Amycolatopsis methanolica.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
OC Amycolatopsis.
OC [1]
RN RN
RP SEQUENCE.
RC STRAIN=NCIB 11946;
RX MEDLINE=96140591; PubMed=8554333;
RA "Kim S.W., Luykx D.M.A.M., de Vries S., Duine J.A.:
RT "A second molybdoprotein aldehyde dehydrogenase from Amycolatopsis
RL methanolica NCIB 11946."
RL Arch. Biochem. Biophys. 325:1-7(1996).
CC -1 SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA
CC CHAIN
KM Oxidoreductase.
KW FT
FT MON_TER 21
SQ SEQUENCE 21 AA; 2208 MW; 193F40E0285A03B0 CRC64;

Query Match 56.5%; Score 26; DB 1; Length 21;
Best Local Similarity 15.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXXVPAPTOXXXXXX 20
   : : : : : | | | : : : :
Db 1 MIPAFDIYAPSTYDEAYOA 20

RESULT 14
BRIA_RANES STANDARD; PRT; 24 AA.
ID BRIA_RANES P40835;
AC P40835;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BREVININ-1EA.
OS Rana esculenta (Edible frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

```

```

DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S19 (FRAGMENT).
GN RPS.
OC Achromatoplasma laldlawii.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Achromatoplasma laldlawii.
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE-92210505; PubMed-1556079;
RA Lim P.O., Sears B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
organism and Achromatoplasma laldlawii deduced from two ribosomal protein
gene sequences."
RL J. Bacteriol. 174:2606-2611(1992).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M74771; AAA21911.1; -
DR PIR: E41839; E41839.
DR INTERPRO: IPR002222; -
DR PRAM: PF00203; RIBOSOMAL_S19; PARTIAL.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2951 MW; 6A9F5F18C6B7A89B CRC64;

Query Match 58.7%; Score 27; DB 1; Length 25;
Best Local Similarity 16.7%; Pred. No. 1.5e+03;
Matches 3; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY 3 XXXXXVPAPTOXXXXXX 20
Db 1 CHKIGFAPTPTFRGCHK 18

RESULT 9
HOXY_NOCOP STANDARD; PRT; 29 AA.
AC P23660;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NAD-REDUCING HYDROGENASE HOXS DELTA SUBUNIT (EC 1.12.1.2) (FRAGMENT).
GN HOXY.
OS Nocardiopsis opaca.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Nocardiaceae; Nocardi.
RN 11)
RP SEQUENCE.
RC STRAIN-1B;
RX MEDLINE-89231684; PubMed-2496982;
RA Zaborosch C., Schneider K., Schlegel H.G., Kratzin H.;
RT "Comparison of the NH2-terminal amino acid sequences of the four non-
identical subunits of the NAD-linked hydrogenases from Nocardiopsis opaca
RT 1b and Alcaligenes eutrophus H16."
RL Eur. J. Biochem. 181:175-180(1989).
CC -1- CATALYTIC ACTIVITY: H(2) + NAD(+) -> H(+) + NADH.
CC -1- COFACTOR: FMN, NICKEL, TWO 4FE-4S, A 3FE-4S, AND A 2FE-2S
CC CLUSTER.
CC -1- SUBUNIT: Tetramer of an alpha and a gamma subunits (flavin-

```

```

CC CONTAINING DIMER), AND A DELTA AND A NICKEL-CONTAINING BETA
SUBUNIT (HYDROGENASE DIMER).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: TO OTHER [NIFE] OR [NIFESE] HYDROGENASES SMALL
SUBUNIT.
CC PIR: S03947; S03947.
DR Oxidoreductase; NAD; Iron-sulfur; 3Fe-4S; Plasmid.
KW Oxidoreductase; NAD; Iron-sulfur; 3Fe-4S; Plasmid.
FT NON_TER 29
SQ SEQUENCE 29 AA; 3159 MW; 1F54BC68F6AED6A CRC64;

Query Match 58.7%; Score 27; DB 1; Length 29;
Best Local Similarity 10.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 14; Mismatches 4; Indels 0; Gaps 0;

QY 1 XXXXXVPAPTOXXXXXX 20
Db 8 EIASHELPTPLDPLVLAAG 27

RESULT 10
LAL1_PIG STANDARD; PRT; 30 AA.
AC P80171;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LIM AND SH3 PROTEIN 1 (LASP-1) (CYSTEINE-RICH PEPTIDE ZF-1)
DE (FRAGMENT).
GN LASP1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
RN 11)
RP SEQUENCE.
RC TISSUE-INTESTINE; PubMed-8425549;
RX MEDLINE-93145972; PubMed-8425549;
RA Sillard R., Joernvall H., Carlquist M., Mutt V.;
RT "Chemical assay for cyst(e)ine-rich peptides detects a novel.
RT intestinal peptide zF-1, homologous to a single zinc-finger motif."
RL Eur. J. Biochem. 211:377-380(1993).
RN 12)
RP STRUCTURE BY NMR.
RX MEDLINE-96438771; PubMed-8841116;
RA Hammarstrom A., Berndt K.D., Sillard R., Ademann K., Otting G.;
RT "Solution structure of a naturally-occurring zinc-peptide complex
RT demonstrates that the N-terminal zinc-binding module of the Lasp-1
RT LIM domain is an independent folding unit."
RL Biochemistry 35:12723-12732(1996).
CC -1- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
IONS.
CC PIR: S28849; S28849.
DR PDB: 1ZPO; 08-NOV-96.
DR INTERPRO: IPR001781; -
DR PFAM: PF00412; LIM_1.
DR PROSITE: PS00478; LIM_DOMAIN_1; PARTIAL.
DR PROSITE: PS50023; LIM_DOMAIN_2; 1.
KW LIM motif; Metal-binding; Zinc; Acetylation; 3D-structure.
FT MOD_RES 1
FT DOMAIN 5 1 ACETYLATION.
FT NON_TER 30
FT DOMAIN 30 >30 LIM.
SQ SEQUENCE 30 AA; 3517 MW; 042AB8FE2314986 CRC64;

Query Match 58.7%; Score 27; DB 1; Length 30;
Best Local Similarity 15.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXVPAPTOXXXXXX 20
Db 4 NCARCGKIVPTPEKVNCLDX 23

```

```

QY      2 xxxxxxxxPVAPVPTQXXXXX 18
Db      1 APEPAPVPVPPAAAAPPV 17
        ::::::::::| :::::

RESULT  7
ODPX_BOVIN
ID      ODPX_BOVIN      STANDARD:      PRT:      22 AA.
AC      P22439;
DT      01-AUG-1991 (Rel. 19, Created)
DT      01-AUG-1991 (Rel. 19, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      PYRUVATE DEHYDROGENASE PROTEIN X COMPONENT (DIHYDROLIPOAMIDE
DE      DEHYDROGENASE-BINDING PROTEIN OF PYRUVATE DEHYDROGENASE COMPLEX) (E3-
DE      BINDING PROTEIN) (E3BP) (FRAGMENT).
GN      PDX1.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bos.
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=89338724; PubMed=2759236;
RA      Neagle J., de Marcucci O., Dunbar B., Lindsay J.G.;
RT      "Component X of mammalian pyruvate dehydrogenase complex: structural
RT      and functional relationship to the lipate acetyltransferase (E2)
RT      component.";
RL      FEBS Lett. 253:11-15(1989).
RN      [2]

```

RA	Rice J.E., Dunbar B., Lindsay J.G.:
RT	"Sequences directing dihydrolipoamide dehydrogenase (E3) binding are located on the 2-oxoglutarate dehydrogenase (E1) component of the mammalian 2-oxoglutarate dehydrogenase multienzyme complex.";
RL	EMBO J. 11:3329-3335(1992).
CC	-1- FUNCTION: REQUIRED FOR ANCHORING DIHYDROLIPOAMIDE DEHYDROGENASE (E3) TO THE DIHYDROLIPOAMIDE TRANSACETYLASE (E2) CORE OF THE PRIVATE DEHYDROGENASE COMPLEXES OF EUKARYOTES. THIS SPECIFIC BINDING IS ESSENTIAL FOR A FUNCTIONAL PDH COMPLEX.
CC	-1- SUBUNIT: EUKARYOTIC PRIVATE DEHYDROGENASE COMPLEXES ARE ORGANIZED ABOUT A CORE CONSISTING OF THE OLIGOMERIC DIHYDROLIPOAMIDE ACETYLTRANSFERASE AROUND WHICH ARE ARRANGED MULTIPLE COPIES OF PRIVATE DEHYDROGENASE, DIHYDROLIPOAMIDE DEHYDROGENASE AND PROTEIN X BOUND BY NONCOVALENT BONDS.
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC	-1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC	-1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
DR	INTERPRO: IPR003016; -
DR	PROSITE: PS00189; LIPOYL; PARTIAL.
KW	Mitochondrion; Lipoyl.
FT	VARIANT 13 P -> G.
FT	NON TER 22
SQ	SEQUENCE 22 AA; 2384 MW; 8985757298279301 CRC64;
Query Match	58.7%; Score 27; DB 1; Length 22;
Best Local Similarity	10.0%; Pred. No. 1,3e+03;
Matches 2; Conservative 16; Mismatches 2; Indels 0; Gaps 0;	
OY	1 XXXXXXXPVPQXXXXXXXXX 20 : : : : : : : : Db 3 PIKILMPSLSEPTMEGNIVK 22
RESULT 8	
RS19_ACHLA	STANDARD;
ID RS19_ACHLA	PRT; 25 AA.
C P29224;	

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE DNA GYRASE SUBUNIT A (EC 5.99.1.3) (FRAGMENT).
 GN GYRA.
 OS Streptomyces sp. *Streptomyces*.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
 NC Actinomycetales; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NCIB 11891.
 RX MEDLINE-93316846; PubMed-8392138.
 RA Thiera A.S., Cundliffe E.;
 RT "Expression and analysis of two gyrb genes from the novobiocin
 RT producer, *Streptomyces sp.*."
 RL Mol. Microbiol. 8:495-506(1993).
 CC -1- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
 CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
 CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
 CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
 CC -1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
 CC OF DOUBLE-STRANDED DNA.
 CC -1- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
 CC BREAKAGE AND REJOINING. THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
 CC ENZYME FORMS AN A2B2 TETRAMER.
 CC -----
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z17305; CAA78953.1; -
 DR KM Topoisomerase: Isomerase; DNA-binding.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA; 2203 MW; 5E2F9DEABDB83697 CRC64;
 SO
 Query Match 67.4%; Score 31; DB 1; Length 21;
 Best Local Similarity 15.8%; Pred. No. 2.6e+02;
 Matches 3; Conservative 14; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 XXXXXXXXVAPQXXXXXX 20
 Db 1 MADDPTVMPVEEPAVEGV 19
 RESULT 3
 ALKB_SALTY STANDARD; PRT; 24 AA.
 AC P37462;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ALKYLATED DNA REPAIR PROTEIN ALKB (FRAGMENT).
 GN ALKB.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 NC Salmonella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91267928; PubMed-1904855;
 RA Hakura A., Morimoto K., Sofuni T., Nohmi T.;
 RT "Cloning and characterization of the *Salmonella typhimurium* ada gene,
 RT which encodes 66-methylguanine-DNA methyltransferase.";
 RL J. Bacteriol. 173:3663-3672(1991).
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE REPAIR OF ALKYLATED DNA.
 CC -----
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D90221; -; NOT_ANNOTATED_CDS.
 DR PIR: B39433; B39433.
 DR STYGENE: SCG10006; ALKB.
 DR DNA repair.
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2780 MW; CBB948C28BF908F3 CRC64;
 SO

Query Match 65.2%; Score 30; DB 1; Length 24;
 Best Local Similarity 16.7%; Pred. No. 4.5e+02;
 Matches 3; Conservative 14; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 XXXXXXXXVAPQXXXXXX 18
 Db 7 DEAPMOEPLAPGRVLR 24

RESULT 4
 TAT_HV1ZH STANDARD; PRT; 30 AA.
 ID TAT_HV1ZH
 AC P12512;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
 GN TAT.
 OS Human immunodeficiency virus type 1 (Zaire HZ321 isolate) (HIV-1).
 OC Viruses; Retrod viruses; Retroviridae; Lentiviruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89228766; PubMed-2713163;
 RA Strinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,
 RA McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
 RT "Molecular characterization of HIV-1 isolated from a serum collected
 RT in 1976: nucleotide sequence comparison to recent isolates and
 RT generation of hybrid HIV.";
 RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 CC -----
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M15896; AAB53949.1; -
 DR HIV: M15896; TAT52321.
 KM Transcription regulation; Activator; RNA-binding; Nuclear protein;
 KW AIDS.
 FT NON_TER 1 1
 SQ SEQUENCE 30 AA; 3329 MW; 545F848858040A1F CRC64;
 SO

Query Match 63.0%; Score 29; DB 1; Length 30;
 Best Local Similarity 10.0%; Pred. No. 8.6e+02;
 Matches 2; Conservative 15; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 XXXXXXXXVAPQXXXXXX 20
 Db 2 LPTTRGPTGPKESKEVES 21

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 12:58:13 ; Search time 12.53 Seconds

(without alignments)
51.547 Million cell updates/sec

Title: US-09-372-036-17

Perfect score: 46

Sequence: 1 XXXXXXXXPPVAPPTQXXXXXX 20

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1785

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	33	71.7	1 IPPD_MOUSE	Q60829 mus musculu
2	31	67.4	21 GYRA_STRSH	P50071 streptomyc
3	30	65.2	24 1 ALKB_SALTY	P37462 salmonella
4	29	63.0	30 1 TAT_HV12H	P15112 human Immun
5	28	60.9	27 1 L52_ADE07	P05663 human adeno
6	27	58.7	17 1 A45K_MYCBO	P80069 mycobacteri
7	27	58.7	22 1 ODPX_BOVIN	P22439 bos taurus
8	27	58.7	25 1 RS19_ACHLA	P22660 echinoplasm
9	27	58.7	29 1 HOXY_MOCOP	P22660 nocardia op
10	27	58.7	30 1 LAS1_PIG	P80171 sus scrofa
11	27	58.7	30 1 Y161_TREPA	O83196 treponema p
12	26	56.5	19 1 TCHI_TRILO	P80070 trichoderm
13	26	56.5	21 1 FDBB_AMEYE	P80706 amycolatos
14	26	56.5	24 1 BR1A_RANES	P40835 rana escul
15	26	56.5	25 1 ARPD_MICU	P80285 micrococci
16	25	54.3	15 1 UC08_MAIZE	P80614 zea mays (m
17	25	54.3	19 1 COOT_SARBU	Q03148 sarcophaga
18	25	54.3	19 1 PSAB_CUCSA	P24047 cucumis sat
19	25	54.3	19 1 UKA1_HUMAN	P31940 homo sapien
20	25	54.3	20 1 FRHA_METBA	P80489 methanosarc
21	25	54.3	23 1 IIP2_PIG	P24853 sus scrofa
22	25	54.3	24 1 THD2_SALTY	P11954 salmonella
23	25	54.3	28 1 COXB_SOLIU	P80499 solanum tub
24	25	54.3	29 1 RP54_CLOKL	P38944 clostridium
25	25	54.3	29 1 SDHB_CLOPR	P80213 clostridium
26	25	54.3	30 1 CY35_DESAC	P81079 desulfuromo
27	25	54.3	19 1 ALL7_OLEEU	P81430 olea europ
28	24	52.2	20 1 DER6_DERPT	P49277 dermatophag
29	24	52.2	25 1 H2B1_ECHRS	P13281 echinus esc
30	24	52.2	25 1 NEUU_CANFA	P34962 canis fami
31	24	52.2	27 1 LIPS_BOVIN	P16386 bos taurus
32	24	52.2	28 1 CIOC_RAT	P13722 ratu
33	24	52.2	28 1 RS19_PHSI	O66093 phytoplasm

34	24	52.2	29	1	CERB_CERCA	P36191 ceratitlis c
35	24	52.2	30	1	FIBR_PANIN	P22775 panulirus i
36	24	52.2	30	1	PAHX_RAT	P57093 rattus novy
37	23	50.0	11	1	BPP_AGRHP	P04562 agkistrodon
38	23	50.0	12	1	FARI_CALVO	P41869 calliphora
39	23	50.0	13	1	UNO2_PINS	P81667 pinus pinas
40	23	50.0	17	1	RM35_YEAST	P36530 saccharomyc
41	23	50.0	20	1	DEF6_DERFA	P49276 dermatophag
42	23	50.0	20	1	PYRR_PYRPH	P37362 pyrrhocoris
43	23	50.0	21	1	CEPA_TREPH	P56738 treponema p
44	23	50.0	24	1	KPKK_CLOPA	P81344 clostridium
45	23	50.0	24	1	LPA2_BACSU	P08497 bacillus su

ALIGNMENTS

RESULT 1	IPPD_MOUSE	STANDARD;	PRT;	27 AA.
AC	Q60829;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	DOPAMINE- AND CAMP-REGULATED NEURONAL PHOSPHOPROTEIN (DARPP-32)			
DE	(FRAGMENT).			
GN	PP1R1B.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BAUB/C;			
RX	MEDLINE=96043524; PubMed=7485543;			
RA	Blau S., Daly L., Fienberg A., Teitelman G., Ehrlich M.E.,			
RT	"DARPP-32 promoter directs transgene expression to renal thick			
RT	ascending limb of loop of Henle."			
RL	Am. J. Physiol. 269:F564-F570(1995).			
CC	-1- FUNCTION: INHIBITOR OF PROTEIN-PHOSPHATASE 1.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- PTM: DOPAMINE- AND CYCLIC AMP-REGULATED NEURONAL PHOSPHOPROTEIN			
CC	(BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE PROTEIN PHOSPHATASE INHIBITOR 1 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
DR	EMBL: U23160; AAA93223.1; "			
KW	Protein phosphatase inhibitor; Acetylation.			
FT	MOD.RES			
FT	NON_TER			
FT	1			
FT	27			
FT	ACETYLATION (BY SIMILARITY).			
SO	SEQUENCE			
	27 AA; 3139 MW; 2FCB2C85F9458444 CRC64;			
Query Match	71.7%;			
Best Local Similarity	15.0%;			
Matches	3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;			
OY	1 XXXXXXXXPPVAPPTQXXXXXX 20			
DB	7 KRIQSVAPPSQDPPOVE 26			
RESULT 2	GYRA_STRSH	STANDARD;	PRT;	21 AA.
ID	P50071;			
AC	01-OCT-1996 (Rel. 34, Created)			

OY 2 XXXXXXPVAPTOXXXXXX 20
: : : : :
Db 1 ADAGTTPAAPATGAGDA 19

RESULT 14

B39433
ada 3'-region alkB homolog - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 30-Sep-1993
C:Accession: B39433
R:Hakura, A.; Morimoto, K.; Sofuni, T.; Nohmi, T.
J. Bacteriol. 173, 3663-3672, 1991
A:Title: Cloning and characterization of the Salmonella typhimurium ada gene, which encodes
A:Accession: B39433; MUID:91267928
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-24 <HAK>
A:Cross-references: GB:D90221
C:Superfamily: alkB protein

Query Match 65.2%; Score 30; DB 2; Length 24;
Best Local Similarity 16.7%; Pred. No. 1.1e+03;
Matches 3; Conservative 14; Mismatches 1; Indels 0; Gaps 0;

OY 1 XXXXXXPVAPTOXXXXXX 18
: : : : :
Db 7 DEAPWQELAPGRVLR 24

RESULT 15

P00369
L protein - rabies virus (isolates PM and CVS)
C:Species: rabies virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 12-Apr-1995
C:Accession: P00369
R:Sacramento, D.; Badrane, H.; Bourhy, H.; Tordo, N.
J. Gen. Virol. 73, 1149-1158, 1992
A:Title: Molecular epidemiology of rabies virus in France: Comparison with vaccine strains
A:Reference number: P00340; MUID:92268873
A:Accession: P00369
A:Molecule type: mRNA
A:Residues: 1-25 <SAC>
C:Superfamily: rhabdovirus L protein

Query Match 65.2%; Score 30; DB 2; Length 25;
Best Local Similarity 10.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 16; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXPVAPTOXXXXXX 20
: : : : :
Db 4 PGDVYDDPIDPIESEAEPRG 23

Search completed: February 13, 2001, 12:59:05
Job time: 77 sec

B49413
perillipin B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C:Accession: B49413
R:Greenberg, A.S.; Egan, J.J.; Mek, S.A.; Moos Jr., M.C.; Londo, C.; Kimmel, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 12035-12039, 1993
A:Title: Isolation of cDNAs for perillipins A and B: sequence and expression of 11p1d drc
A:Reference number: A49413; MUID:94089764
A:Accession: B49413
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-26 <GRE>
A:Experimental source: adipocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:141052, NCBI:141054)

Query Match 69.6%; Score 32; DB 2; Length 26;
Best Local Similarity 15.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXPVAPTOXXXXXX 20
:::|||||:::
DB 3 DTVVHYVPSPAPGPPSDQ 22

RESULT 9
S32883
DNA gyrase chain A - Streptomyces spheroides (fragment)
C:Species: Streptomyces spheroides
C:Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 22-Oct-1999
C:Accession: S32883; S29684
R:Thiara, A.S.; Cundliffe, E.
Mol. Microbiol. 8, 495-506, 1993
A:Title: Expression and analysis of two gyrb genes from the novobiocin producer, Strepto
A:Reference number: S32881; MUID:93316846
A:Accession: S32883
A:Molecule type: DNA
A:Residues: 1-21 <THL>
A:Cross-references: EMBL:Z17305; NID:g47535; PIDN:CAA78953.1; PID:g47537

Query Match 67.4%; Score 31; DB 2; Length 21;
Best Local Similarity 15.8%; Pred. No. 6.3e+02;
Matches 3; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

OY 2 XXXXXXXPVAPTOXXXXXX 20
:::|||||:::
DB 1 MADENTPWPEVPAVEGV 19

RESULT 10
S41390
p7 protein - human adenovirus 3 (fragment)
C:Species: Mastadenovirus h3 (human adenovirus 3)
C:Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 08-Oct-1999
C:Accession: S41390
R:Cuzange, A.; Chroboczek, J.; Jacrot, B.
submitted to the EMBL Data Library, January 1994
A:Description: The penton base of human adenovirus type 3 has the RGD motif.
A:Reference number: S41388
A:Accession: S41390
A:Molecule type: DNA
A:Residues: 1-23 <CUZ>
A:Cross-references: EMBL:Z29487; NID:g444048; PIDN:CAA82623.1; PID:g444051
A:Experimental source: serotype 3

Query Match 67.4%; Score 31; DB 2; Length 23;
Best Local Similarity 15.0%; Pred. No. 7e+02;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXPVAPTOXXXXXX 20

DB 3 PPRCMEAPASSTQHPVRRV 22
:::|||||:::
RESULT 11
S06966
Hypothetical protein (nifa 3' region) - Rhizobium leguminosarum (fragment)
C:Species: Rhizobium leguminosarum
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999
C:Accession: S06966
R:Roelink, P.W.; Hontela, J.G.J.; van Kammen, A.; van den Bos, R.C.
Mol. Microbiol. 3, 1441-1447, 1989
A:Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum p
A:Reference number: S06964; MUID:90136072
A:Accession: S06966
A:Molecule type: DNA
A:Residues: 1-30 <ROE>
A:Cross-references: EMBL:X17073; NID:g46208; PIDN:CAA34925.1; PID:g46211

Query Match 67.4%; Score 31; DB 2; Length 30;
Best Local Similarity 16.7%; Pred. No. 9.5e+02;
Matches 3; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

OY 1 XXXXXXXPVAPTOXXXXX 18
:::|||||:::
DB 13 SAPSDRAPWAPMPCGAA 30

RESULT 12
J00356
Cycloleoneurinin - sagebrush motherwort
C:Species: Leonurus artemisia (sagebrush motherwort)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: J00356
R:Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.
Chem. Pharm. Bull. 39, 712-715, 1991
A:Title: Cycloleoneurinin, a cyclic peptide from Leonuri fructus.
A:Reference number: J00356; MUID:91300597
A:Accession: J00356
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIN>

Query Match 65.2%; Score 30; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 4.8e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 6 XXPVAPTOXXXX 17
:::|||||:::
DB 1 YTPAGPTGYPPY 12

RESULT 13
S38291
30K allergen - velvet grass (fragment)
C:Species: Holcus lanatus (velvet grass)
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 19-May-2000
C:Accession: S38291
R:Peterson, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
A:Title: Comparison of four grass pollen species concerning their allergens of grass
A:Reference number: S38288; MUID:94092339
A:Accession: S38291
A:Molecule type: protein
A:Residues: 1-20 <PET>

Query Match 65.2%; Score 30; DB 2; Length 20;
Best Local Similarity 15.8%; Pred. No. 8.7e+02;
Matches 3; Conservative 13; Mismatches 3; Indels 0; Gaps 0;


```

QY      1 xxxxxxxxPAPProxxxx 19
        : : : : : | | | : : : :
Db      2 LAFHDISPQAPPTHFLVIR 20
Matches 4; Conservative 13; Mismatches 2; Indels 0; Gaps 0.

```

RESULT 3
C24536
alpha-amylase/trypsin inhibitor CMC - barley (fragment)
C: Spoiled; Hardwood (H) (zero; (below))

C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 07-Feb-1997
C:Accession: C24536
R:Barber, D.; Sanchez-Monge, R.; Mendez, E.; Lazaro, A.; Garcia-Olmedo, F.; Salcedo, G.
R:Biochim. Biophys. Acta 869, 115-118, 1986
A:Title: New alpha-amylase and trypsin inhibitors among the CM-proteins of barley (Hordeum vulgare L.)
A:Reference number: A90658; MUID:86104339
A:Accession: C24536
A:Molecule type: protein
A:Residues: 1-29 <BAR>
C:Superfamily: wheat alpha-amylase inhibitor
C:Keywords: alpha-amylase inhibitor

Query Match	73.98	Score 34	DB 2	Length 29
Best Local Similarity	20.08	Pred. No.	2.9e+02	
Matches	4	Conservative	2	Indels 0; Gaps 0;
		Mismatches	2	

```
Oy 1 XXXXXXXXPVAP7QXXXXXXXXX 20
    : : : : : | | : : : : :
Db 6 CYEGMGLPVNPLQGCRFYVA 25
```

RESULT	4
G39690	

C:Neural cell adhesion molecule, catenac splice form 1, 1-745 aa (Norway rat) (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 C:Accession: G39690
 R:Reyes, A.A.; Small, S.T.; Akeson, R.
 M:1. Cell. Biol. 11, 1654-1661, 1991
 A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
 A:Reference number: A39690; MUID:91141516
 A:Accession: G39690
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-29 <REV>
 A:Cross-references: GB:M63970
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin
 C:Keywords: cardiac muscle; cell adhesion; heart

```

Query Match      71.7%  Score 33; DB 2; Length 29;
Best Local Similarity 15.0%  Pred. No. 4.3e+02;
Matches 3; Conservative 15; Mismatches 2; Indels 0; Gaps 0.

Qy 1 xxxxxxxxpyapTQxxxxxxx 20
    : : : : : : : : : : : : : : : :
Db . 1 OPVHSPPLAPLANSSTLVLPL 20

```

RESULT 5

P11790
 T cell receptor alpha chain V region (clone 2BBL V alpha 24-6) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: P11790

A:Title: Analyls of T cell antigen receptor (TCR) expression by human peripheral blood
A:Reference number: PH1754; MUID:93301585

A;Accession: PH1790
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 <P>

Query Match	69.6%	Score	32	DB	2	Length	16
Best Local Similarity	18.8%	Pred. No.	3.1e+02				
Matches	3	Conservative	11	Mismatches	2	Indels	0
						Gaps	0

```

OY      1 XXXXXXXXPVAPTQXXX 16
        :::::::::::| | :::
Db      1 HLCGERPITPTSSSL 16

```

RESULT
F61491

C:Accession: F61491
C:Species: *Psophocarpus tetragynolobus* (Winged bean)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 03-May-1996
C:Accession: F61491
C:Author: R.Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two
A:Reference number: A61491; MUID:89351606
A:Accession: F61491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <Hir>
C:Superfamily: pathogenesis-related protein
C:Keywords: seed

```

69.6%; Score 32; DB 2; Length 23;
Best Local Similarity 26.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
QY 1 XXXXXXXXPVAPLQXXXXXX 19
    ::::||||| ::::
db 5 YEDFTTXPVAPAPILTKAIV 23

```

RESULT	7
I39289	

Z.F.3 domain - numan (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 02-Aug-1996 #sequence_rev:0100 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: J39289
 R:Gawra, O.; Eccles, M.R.; Yun, K.; Mueller, R.F.; Holdaway, M.D.; Reeve, A.E.
 Hum. Mol. Genet. 2, 203-204, 1993
 A:Title: A novel insertional mutation at the third zinc finger coding region of the W
 A:Reference number: J39288; MUID:93271969
 A:Accession: J39289
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-24 <RES>
 A:Cross-references: EMBL:X72323; NID:g312851; PIDN:CAA51062.1; PID:g312852
 C:Genetics:
 A:Gene: GDB:WT1
 A:Cross-references: GDB:120496; OMIM:194070
 A:Map position: 11p13-11p13

Query match	69.68;	Score 32;	DB 2;	Length 24;
-------------	--------	-----------	-------	------------

	Matches	· 3;	Conservative	15;	Mismatches	2;	Indels	0;	Gaps	0.
QY	1	XXXXXXXXXX	PATQXXXXXXX	20						
								
Db	· 4	NLSAKVLPVRPPEDH	QDSDY	23						

RESULT 8

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 12:57:48 ; Search time 20.45 Seconds
(without alignments)
66.407 Million cell updates/sec

Title: US-09-372-036-17

Perfect score: 46
Sequence: 1 xxxxxxxxPVAPPTQxxxxxx 20

Scoring table: BL0SUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 6242

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	73.9	18	2	A28027
2	34	73.9	20	2	S72501
3	34	73.9	29	2	C24536
4	33	71.7	29	2	G39690
5	32	69.6	16	2	PH1790
6	32	69.6	23	2	F61491
7	32	69.6	24	2	I39289
8	32	69.6	26	2	B49413
9	31	67.4	21	2	S32883
10	31	67.4	23	2	S41390
11	31	67.4	30	2	S06966
12	30	65.2	12	2	JU0356
13	30	65.2	20	2	S38291
14	30	65.2	24	2	B39433
15	30	65.2	25	2	P00369
16	30	65.2	25	2	S52124
17	30	65.2	28	2	A25310
18	29	63.0	19	2	B38837
19	29	63.0	20	2	T44453
20	29	63.0	24	2	A61505
21	29	63.0	25	2	A30590
22	29	63.0	27	2	B60704
23	29	63.0	27	2	B37043
24	29	63.0	28	2	C56262
25	29	63.0	28	2	S56121
26	29	63.0	28	2	T37143
27	29	63.0	29	1	TNLJBR
28	29	63.0	30	2	S74112
29	28	60.9	14	2	PH1806

30	28	60.9	20	2	I46940	6-phosphofructo-2-
31	28	60.9	20	2	A25335	myosin-light-chain
32	28	60.9	24	2	T42258	ser/tnr protein ph
33	28	60.9	24	2	S53793	actin - mouse (fra
34	28	60.9	27	2	A24487	aldose 1-epimerase
35	28	60.9	28	2	JN0366	proteinase inhibit
36	28	60.9	29	2	PC4429	peroxisome prolif
37	28	60.9	30	2	C61233	conceptus protein
38	28	60.9	30	2	S55462	mer5 protein homol
39	28	60.9	30	2	B60291	30k serine protein
40	27	58.7	17	2	A49237	45/47k antigen - M
41	27	58.7	17	2	S33609	extensin - maize (
42	27	58.7	18	2	S56715	hydroxymethylgluta
43	27	58.7	20	2	S59494	formate dehydrogen
44	27	58.7	21	2	C39543	collagen alpha 3(I
45	27	58.7	21	2	P28027	protein p9 - curle

ALIGNMENTS

RESULT 1
A28027
protein p2 - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C:Date: 19-May-1989 #sequence #revision 19-May-1989 #text_change 18-Jun-1993
C:Accession: A28027
R:Baum, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino ac
A:Reference number: A94167
A:Accession: A28027
A:Molecule type: protein
A:Residues: 1-18 <DAU>
A>Note: 14-Arg was also found

Query Match 73.9%; Score 34; DB 2; Length 18;
Best Local Similarity 31.2%; Pred. NO. 1.7e+02;
Matches 5; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 xxxxxxxxPVAPPTQxxxx 16
DB 3 SKXDTIVPAPQNLV 18

RESULT 2
S72501
protein kinase C inhibitor - human (fragment)
N:Alternate names: histidine triad nucleotide-binding protein
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence #revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S72501; S62623
R:Maines, M.D.; Trakshel, G.M.
Arch. Biochem. Biophys. 300, 320-326, 1993
A:Title: Purification and characterization of human biliverdin reductase.
A:Reference number: S29736; MUID:93143333
A:Accession: S72501
A:Molecule type: protein
A:Residues: 1-20 <MAT>
A>Note: This protein was identified as biliverdin reductase; the identification is qu
R:Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Eur. J. Biochem. 235, 372-381, 1996
A:Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati
A:Reference number: S62622; MUID:96202961
A:Accession: S62623
A:Molecule type: protein
A:Residues: 1-20 <MAW>
C:Superfamily: protein kinase C inhibitor; histidine triad homology
C:Keywords: homodimer; protein kinase inhibitor; zinc

Query Match 73.9%; Score 34; DB 2; Length 20;


```

APPLICANT: NEUMANN, STEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-26

Query Match 76.1%; Score 35; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. NO. 1.3e+05;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 XXXPVAPPTQ 13
:::|||||
DB 1 VSTPVAPPTQ 9

```

```

APPLICANT: Anderson, W. French
APPLICANT: Wu, Bonnie W.
TITLE OF INVENTION: Retroviral Envelopes Having
TITLE OF INVENTION: Modified Hypervariable polypollone Regions
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: Carella, Byrne, Bain, Giffillan, Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,074A
FILING DATE: 14-May-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 271010-378
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-856-074A-34

Query Match 76.1%; Score 35; DB 3; Length 26;
Best Local Similarity 20.0%; Pred. NO. 1e+02;
Matches 4; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

QY 1 XXXXXXXPVAPPTQXXXXX 20
:::|||||
DB 3 RVPICPNVLPDQRLPSSPI 22

RESULT 15
US-07-794-288D-91
Sequence 91, Application US/07794288D
Patent No. 5580953
GENERAL INFORMATION:
APPLICANT: ELISABETH ALBRECHT,
APPLICANT: HOWARD JONES,
APPLICANT: LAURA S.L. GAETA,
APPLICANT: KATHRYN S. PRICKETT and
APPLICANT: KEVIN BEAUMONT
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESS: LYON & LYON
STREET: First Interstate World
STREET: Center
STREET: 633 West Fifth Street,
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

```

Matches 4; Conservative 14; Mismatches 2; Indels 0; Gaps 0;
Qy 1 XXXXXXXXVAPTOXXXXXX 20
Db 8 PSMVEEPAPAPOLPKRIS 27

RESULT 11

US-08-456-670B-31
; Sequence 31, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINWELLER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BOBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE: Listeria monocytogenes
; STRAIN: EGD
; US-08-456-670B-31

Query Match 78.3%; Score 36; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVAPTOXXXX 17
Db 1 PVAPTOEVKK 10

RESULT 12

US-08-908-643C-29
; Sequence 29, Application US/08908643C
; Patent No. 6120995
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; Pearlman, Joshua M.
; Barber, Michael T.
; Schultz, Stephanie
; Parkinson, Scott J.
; TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO
; COLORECTAL CANCER CELLS AND METHODS OF
; USING THE SAME
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995rls LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,643C
; FILING DATE: 07-Aug-1997
; CLASSIFICATION: N/A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark DeLuca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-08-908-643C-29

Query Match 78.3%; Score 36; DB 3; Length 19;
Best Local Similarity 15.8%; Pred. No. 47;
Matches 3; Conservative 15; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XXXXXXXXVAPTOXXXXXX 19
Db 1 MLMRLAPFISPTNSALRWC 19

RESULT 13
US-08-456-670B-26
; Sequence 26, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER

RESULT 9
US-08-143-365A-6
Sequence 6, Application US/08143365A
Patent No. 5726292
GENERAL INFORMATION:
APPLICANT: Lowell, George H
TITLE OF INVENTION: IMMUNO-POTENTIATING SYSTEMS FOR
TITLE OF INVENTION: PREPARATION OF IMMUNOGENIC MATERIALS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street
CITY: Fallsfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,365A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535

RESULT 10
 US-08-942-423-9
 : Sequence 9, Application US/08942423
 : Patent No. 5891673
 :
 : GENERAL INFORMATION:
 : APPLICANT: Hashimoto, Yasuhito
 : APPLICANT: Takemoto, Yoshihito
 : TITLE OF INVENTION: Lck Binding Protein
 : NUMBER OF SEQUENCES: 68
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Syntex (U.S.A.) Inc.
 : STREET: 3401 Hillview Ave.
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 94303
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/942,423
 : FILING DATE: 01-OCT-1997
 :
 : CLASSIFICATION: 435
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/362,715
 : FILING DATE: 23-DEC-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Perles, Rohan
 :
 : REGISTRATION NUMBER: 35,752
 : REFERENCE/DOCKET NUMBER: 28260
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 852-1698
 : TELEFAX: (415) 496-3529
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 28 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: not relevant
 : TOPOLOGY: not relevant
 : MOLECULE TYPE: peptide
 :
 : US-08-942-423-9

APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: In Trichoderma
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,951
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: both
FEATURE:
NAME/KEY: Peptide
LOCATION: 17
OTHER INFORMATION: /label= Peptide
OTHER INFORMATION: /note= "The amino acid at position 17 may also be
US-07-923-724-43

Query Match 82.6%; Score 38; DB 1; Length 20;
Best Local Similarity 21.1%; Pred. NO. 26;
Matches 4; Conservative 14; Mismatches 1; Indels 0; Gaps 0;

OY 1 XXXXXXPVAPTOXXXXX 19
Db 2 YHGAGNPLGPTQGVGANE 20

RESULT 7
US-08-609-426A-43
Sequence 43, Application US/08609426A
Patent No. 5830733
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Olmonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.

APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: In Trichoderma
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: both
FEATURE:
NAME/KEY: Peptide
LOCATION: 17
OTHER INFORMATION: /label= Peptide
OTHER INFORMATION: /note= "The amino acid at position 17 may also be
US-08-609-426A-43

Query Match 82.6%; Score 38; DB 2; Length 20;
Best Local Similarity 21.1%; Pred. NO. 26;
Matches 4; Conservative 14; Mismatches 1; Indels 0; Gaps 0;

OY 1 XXXXXXPVAPTOXXXXX 19
Db 2 YHGAGNPLGPTQGVGANE 20

RESULT 8
US-08-969-721-3
Sequence 3, Application US/086969721
Patent No. 5972339
GENERAL INFORMATION:
APPLICANT: Walker, Bruce D.
TITLE OF INVENTION: METHODS OF ELICITING ANTI-HIV-1
TITLE OF INVENTION: HELPER T CELL RESPONSES

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
FEATURE:
OTHER INFORMATION: MAY BE ABSENT"
NAME/KEY: Modified-site
LOCATION: 14-20
OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
US-08-456-670B-17

Query Match 100.0%; Score 46; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 XXXXXXXXVAPTOXXXXXX 20
Db 1 XXXXXXXXVAPTOXXXXXX 20

RESULT 2
US-08-127-499A-27
Sequence 27, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-27

Query Match 93.5%; Score 43; DB 1; Length 21;
Best Local Similarity 35.3%; Pred. No. 5.1;
Matches 6; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

OY 4 XXXXVAPTOXXXXXX 20
Db 1 AVSTVAPTOEVKKETT 17

RESULT 3
US-08-482-847-27
Sequence 27, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 514
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-27

Query Match 93.5%; Score 43; DB 1; Length 21;
Best Local Similarity 35.3%; Pred. No. 5.1;
Matches 6; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

OY 4 XXXXVAPTOXXXXXX 20
Db 1 AVSTVAPTOEVKKETT 17

RESULT 4
US-08-374-652C-32
Sequence 32, Application US/08374652C
Patent No. 5834286
GENERAL INFORMATION:
APPLICANT: NEVALAINEN, HELENA K.M.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OH protein - protein search, using sw model

Run on: February 13, 2001, 12:57:44 ; Search time 19.09 Seconds

(without alignments)
18.813.Million cell updates/sec

Title: US-09-372-036-17

Perfect score: 46

Sequence: 1 xxxxxxxxpvaprtqxxxxxx 20

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

111283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/PCrus.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	20	2	US-08-456-670B-17
2	43	93.5	21	1	US-08-127-499A-27
3	43	93.5	21	1	US-08-482-847-27
4	39	84.8	24	2	US-08-374-652C-32
5	38	82.6	12	2	US-08-456-670B-30
6	38	82.6	20	1	US-07-923-724-43
7	38	82.6	20	2	US-08-609-426A-43
8	38	82.6	22	2	US-08-969-721-3
9	38	82.6	30	1	US-08-143-365A-6
10	37	80.4	28	2	US-08-942-423-9
11	36	78.3	10	2	US-08-456-670B-31
12	36	78.3	19	3	US-08-908-643C-29
13	35	76.1	9	2	US-08-456-670B-26
14	35	76.1	26	3	US-08-856-074A-34
15	35	76.1	29	1	US-07-794-288D-91
16	35	76.1	30	2	US-08-456-670B-31
17	35	76.1	30	2	US-08-399-411-84
18	35	76.1	30	3	US-08-516-859A-84
19	34	73.9	18	4	US-08-205-938A-22
20	34	73.9	18	4	PCT-US95-02626-22
21	34	73.9	20	1	US-08-218-025A-52
22	34	73.9	21	1	US-08-127-499A-33
23	34	73.9	21	1	US-08-482-847-33
24	34	73.9	21	1	US-08-856-074A-35
25	34	73.9	22	1	US-08-218-025A-110
26	34	73.9	22	1	US-08-218-025A-143
27	33	71.7	15	2	US-08-116-733-15
28	33	71.7	15	2	US-08-484-905-30

29	33	71.7	15	3	US-08-481-965B-30	Sequence 30, Appl
30	33	71.7	15	3	US-08-370-476-30	Sequence 30, Appl
31	33	71.7	19	3	US-08-779-764A-33	Sequence 33, Appl
32	33	71.7	21	1	US-08-218-025A-147	Sequence 147, App
33	33	71.7	21	3	US-08-750-419A-5	Sequence 5, Appl
34	33	71.7	25	2	US-08-473-475A-20	Sequence 20, Appl
35	33	71.7	26	2	US-08-389-011-7	Sequence 7, Appl
36	33	71.7	26	3	US-08-403-917A-7	Sequence 11, Appl
37	33	71.7	30	1	US-07-901-874B-11	Sequence 3, Appl
38	33	71.7	30	1	US-08-457-865-11	Sequence 3, Appl
39	33	71.7	30	1	US-08-416-478A-3	Sequence 3, Appl
40	33	71.7	30	2	US-08-474-988B-3	Sequence 3, Appl
41	33	71.7	30	2	US-08-394-442B-3	Sequence 3, Appl
42	32	69.6	14	2	US-08-374-652C-12	Sequence 12, Appl
43	32	69.6	15	1	US-07-923-724-20	Sequence 20, Appl
44	32	69.6	15	1	US-07-923-724-20	Sequence 20, Appl
45	32	69.6	15	2	US-08-609-426A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-456-670B-17
Sequence 17, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: KOEBEL, WERNER
APPLICANT: KOEHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

This Page Blank (uspto)

THIS PAGE BLANK (USPTO)

QY 1 XXXXXXXXPVAPTOXXXXXXXX 20

CC provide a broader population coverage of MHC-reactive alleles.

```

XX  Brewer LA, Ebner R, Ferrle AM, Feng P, Greene JM, Lafleur DW;
PI  Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
PI  Yu GL;
XX  MPI: 1999-080881/07.
DR  N-PSDB: X04315.
XX
PT  New isolated human genes and the secreted polypeptides they encode -
PT  useful for diagnosis and treatment of e.g. cancers, neurological
PT  disorders, immune diseases, inflammation or blood disorders
XX
PS  Claim 11; Page 266; 380pp; English.
XX
XX  This sequence represents a secreted human protein encoded by the gene
CC  clone detailed in the descriptor line. The gene can be used to generate
CC  fusion proteins by linking to the gene to a human immunoglobulin Fc
CC  portion (e.g. X04302) for increasing the stability of the fused protein
CC  as compared to the human protein only.
CC  The invention relates to 86 novel genes and their fragments (nucleic acid
CC  sequences: X04311-X04410; amino acid sequences W78126-W78225) which
CC  are useful for preventing, treating or ameliorating medical conditions
CC  e.g. by protein or gene therapy. Also, pathological conditions can be
CC  diagnosed by determining the amount of the new polypeptides in a sample
CC  or by determining the presence of mutations in the new polynucleotides.
CC  Specific uses are described for each of the 86 polynucleotides, based on
CC  which tissues they are most highly expressed in (see X04311 for described
CC  uses).
XX
SQ  Sequence 27 AA;

```

Query Match 93.5%; Score 43; DB 20; Length 27;
 Best Local Similarity 25.0%; Pred. No. 13;
 Matches 5; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

```

QY  1 XXXXXXXPVAPTOXXXXXX 20
    ::::::::::::::::::::
DB  2 ltfllfpvpletsqknrs 21

```

RESULT 4
 R45172
 ID R45172 standard; Protein; 12 AA.
 AC R45172;
 XX
 DT 16-JUN-1994 (first entry)
 DE Listeria p60 peptide epitope.
 XX
 KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR MPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for

```

PT  immunochemical detection
XX
XX  Disclosure; Fig 2; 19pp; German.
XX
XX  The sequence is that of a Listeria p60 peptide epitope which
CC  which may be used in the prodn. of antibodies for the detection
CC  of Listeria by immunoassay (partic. ELISA). It may be used as
CC  part of a method that allows determination of individual Listeria
CC  species, esp. L. monocytogenes.
XX
SQ  Sequence 12 AA;

```

Query Match 82.6%; Score 38; DB 14; Length 12;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

QY  6 XXPVAPTOXXXX 17
    ::::::::::::::::::::
DB  1 stpvaptdgvvk 12

```

RESULT 5
 R46816
 ID R46816 standard; Protein; 20 AA.
 AC R46816;
 XX
 DT 19-AUG-1994 (first entry)
 DE Phytase derived peptide 792.
 XX
 KW pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid;
 KW phytate degrading enzyme; PDE; removal; inositol hexaphosphoric acid;
 KW plant; feed composition; filtration.
 XX
 OS Synthetic.
 XX
 FI Key Location/Qualifiers
 FT Misc-difference 17
 FT /Label= Gly, Tyr
 XX
 PN W09403612-A.
 XX
 PD 17-FEB-1994.
 XX
 PF 30-JUL-1993; 93WO-FI00310.
 XX
 PR 31-JUL-1992; 92US-0923724.
 XX
 PA (ALKO-) ALKO LTD.
 XX
 PI Cantrell M, Fagerstrom RB, Miettinen-Oinonen ASK;
 PI Nevalainen HK, Paloheimo MT, Piddington C, Ramosek JA;
 PI Torikelli TK, Turunen MK;
 XX
 DR MPI: 1994-065700/08.
 XX
 PT Compsns. contg. phytate degrading enzymes - obtd. by expression
 PT of their genes in Trichoderma, used partic. for producing animal
 PT feed compsns.
 XX
 PS Example 4; Page 44; 142pp; English.
 XX
 CC The sequences given in R46793-824 are peptides derived from the
 CC phytase protein. The phytase protein may be used in the composition
 CC of the invention. The DNA encoding the phytase protein may be
 CC introduced into a Trichoderma host which then expresses it and the
 CC protein is collected from the culture medium. By using Trichoderma as
 CC a host for Aspergillus phytate degrading enzymes such as this, a
 CC totally different enzyme composition compared to that secreted from
 CC Aspergillus results. The enzyme composition can be used for removal
 CC of phytic acid or inositol hexaphosphoric acid from raw material,

XX New primers for PCR detection of *Listeria* - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PS Claim 3: Page 4: 19pp: German.
 XX
 CC The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 XX
 SQ Sequence 20 AA:
 QY
 Query Match 100.0%; Score 46; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 xxxxxxxxvavpTQxxxxxx 20
 ||||||||||||||||
 1 xxxxxxxxvavpTQxxxxxx 20
 RESULT 2
 R73891
 ID R73891 standard; peptide: 21 AA.
 XX
 AC R73891:
 XX
 DT 05-DEC-1995 (first entry)
 XX
 DE *Listeria* monocytogenes protein p60 precursor peptide 144-164.
 XX
 KM *Listeria* monocytogenes; protein p60 precursor; vaccine;
 KM meningitis related homologous antigenic sequence; MRHAS: RV-1;
 KM immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KM viral; peptide 144-164.
 XX
 OS *Listeria* monocytogenes.
 XX
 PN WO9509232-A.
 XX
 PD 06-APR-1995.
 XX
 PF 28-SEP-1994; 94WO-CA00516.
 XX
 PR 28-SEP-1993; 93US-0127499.
 XX
 PA (SHAR/) SHARMA L. R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 PI Sharma LR, Van Alstyne D;
 XX
 DR WPI; 1995-147431/19.
 XX
 PT New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 PS Claim 34: Page 74; 98pp: English.
 XX
 CC R73913 is the *Listeria* monocytogenes protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in R73891-R73894 and R73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 XX

SQ Sequence 21 AA:
 QY
 Query Match 93.5%; Score 43; DB 16; Length 21;
 Best Local Similarity 35.3%; Pred. No. 9.1;
 Matches 6; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
 Db 4 xxxxxvavpTQxxxxxx 20
 :|||:|||||:|||||:
 1 avspvavpTQevkkett 17
 RESULT 3
 ID W78130
 W78130 standard; Protein; 27 AA.
 XX
 AC W78130;
 XX
 DT 13-APR-1999 (first entry)
 XX
 DE Human secreted protein encoded by gene 5 clone HPBDD36.
 XX
 KM Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KM inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 FH key Location/Qualifiers
 FT Misc-difference 27
 XX /label= unknown
 PN WO9856804-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 11-JUN-1998; 98WO-US12125.
 XX
 PR 02-OCT-1997; 97US-0061060.
 PR 13-JUN-1997; 97US-0049547.
 PR 13-JUN-1997; 97US-0049548.
 PR 13-JUN-1997; 97US-0049549.
 PR 13-JUN-1997; 97US-0049550.
 PR 13-JUN-1997; 97US-0049606.
 PR 13-JUN-1997; 97US-0049607.
 PR 13-JUN-1997; 97US-0049608.
 PR 13-JUN-1997; 97US-0049609.
 PR 13-JUN-1997; 97US-0049610.
 PR 13-JUN-1997; 97US-0049611.
 PR 13-JUN-1997; 97US-0050566.
 PR 13-JUN-1997; 97US-0050901.
 PR 13-JUN-1997; 97US-0052989.
 PR 08-JUL-1997; 97US-0051919.
 PR 18-AUG-1997; 97US-0055984.
 PR 12-SEP-1997; 97US-0058665.
 PR 12-SEP-1997; 97US-0058668.
 PR 12-SEP-1997; 97US-0058669.
 PR 12-SEP-1997; 97US-0058750.
 PR 12-SEP-1997; 97US-0058971.
 PR 12-SEP-1997; 97US-0058972.
 PR 12-SEP-1997; 97US-0058975.
 PR 02-OCT-1997; 97US-0060834.
 PR 02-OCT-1997; 97US-0060841.
 PR 02-OCT-1997; 97US-0060844.
 PR 02-OCT-1997; 97US-0060865.
 PR 02-OCT-1997; 97US-0061059.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 12:57:45 : Search time 25.91 Seconds
(without alignments)
26.394 Million cell updates/sec

Title: us-09-372-036-17

Perfect score: 46

Sequence: 1 XXXXXXXPVAPTXXXXXXX 20

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 151408

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_36:*

1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT:*

9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT:*

10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	20	14 R45159	Listeria p60 pepti
2	43	93.5	21	16 R73891	Listeria monocytog
3	43	93.5	27	20 W78130	Human secreted pro
4	38	82.6	12	14 R45172	Listeria p60 pepti
5	38	82.6	20	15 R46816	Phytase derived pe
6	38	82.6	22	20 Y04031	HIV-1 p24 peptide
7	38	82.6	22	21 Y73163	HIV-derived MHC cl
8	38	82.6	25	19 W82515	HIV-1 p24 epitope
9	38	82.6	30	19 W44257	Trypanosomal pepti
10	38	82.6	30	19 W45530	Trypanosomal pepti
11	37	80.4	28	20 Y03800	Murine LckBp1 pept
12	37	80.4	30	21 Y69503	C-terminus of MMLV

13	36	78.3	10	14 R45173	Listeria p60 pepti
14	36	78.3	19	20 Y00963	CfCA-1 protein seq
15	35	76.1	9	14 R45168	Listeria p60 pepti
16	35	76.1	22	18 W15790	Human metastasis s
17	35	76.1	26	20 W88517	Amphotropic hyperp
18	35	76.1	28	19 W44919	Spacer peptide for
19	35	76.1	29	7 P61306	Trans-acting trans
20	35	76.1	29	19 W44926	Pro-rich spacer fo
21	34	73.9	18	16 R83666	Insect haemolymph
22	34	73.9	20	17 W08032	HIV peptide #17
23	34	73.9	21	16 R73894	Listeria monocytog
24	34	73.9	21	20 W88518	Amphotropic hyperp
25	34	73.9	22	14 R41293	Peptide fragment F
26	34	73.9	22	17 W07996	gp120 peptide 61.
27	34	73.9	22	17 W07944	gp120 peptide P061
28	34	73.9	23	14 R41294	Peptide fragment F
29	34	73.9	25	14 R42666	HIV gp120 constant
30	34	73.9	27	19 W71104	Amino-terminal pep
31	33	71.7	15	11 W1929	Synthetic peptide
32	33	71.7	15	14 R34237	HIV-II envelope g
33	33	71.7	15	16 R68772	Cytotoxic T lympho
34	33	71.7	15	19 W68321	MHC binding peptid
35	33	71.7	15	19 W63057	Human immunodefici
36	33	71.7	15	21 Y68198	Altered MHC determ
37	33	71.7	15	21 Y52852	Altered MHC determ
38	33	71.7	16	18 W25392	PLC gamma SH3 doma
39	33	71.7	19	19 W30686	Human Borra diseas
40	33	71.7	19	20 Y07480	HIV envelope prote
41	33	71.7	20	19 W71103	Amino-terminal pep
42	33	71.7	21	10 P90332	Amino acids 254-27
43	33	71.7	21	16 P90631	Human immunodefici
44	33	71.7	21	10 R81876	Chloroperoxidase t
45	33	71.7	21	16 R81870	C. Inaequalis chlo

ALIGNMENTS

RESULT 1	
ID R45159	standard; Protein; 20 AA.
AC R45159;	
DT 16-JUN-1994	(first entry)
XX	
DE Listeria p60 peptide epitope.	
XX	
KW Listeria monocytogenes; antibodies; immunosassay; conjugate.	
XX	
OS Synthetic.	
XX	
FI	
FT Key	Location/Qualifiers
FT Region	1..7
FT Region	/note= "opt. 0-7 amino acid residues"
FT Region	14..20
FT Region	/note= "opt. 0-7 amino acid residues"
XX	
PN	
XX	
DE418450-A.	
PD 16-DEC-1993.	
XX	
PF 03-JUN-1993;	93DE-4318450.
XX	
PR 11-JUN-1992;	92DE-4239111.
PR 25-NOV-1992;	92DE-4239567.
XX	
PA (MERCK) MERCK PATENT GMBH.	
XX	
PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;	
PI Hofmann G, Bubert A, Goebel W, Koehler S;	
XX	
DR WPI: 1993-406956/51.	

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:00:39 ; Search time 44.34 Seconds
(without alignments)
6.941 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 45
Sequence: 1 VSTPVAPRQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 151408

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

_A_Geneseq_36: *
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT: *
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT: *
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT: *
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT: *
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT: *
6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT: *
7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT: *
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT: *
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT: *
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT: *
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT: *
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT: *
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT: *
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT: *
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT: *
16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT: *
17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT: *
18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT: *
19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT: *
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT: *
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	45	100.0	9	14 R45168
2	45	100.0	21	16 R73891
3	41	91.1	12	14 R45172
4	32	71.1	6	14 R54615
5	32	71.1	10	14 R45173
6	32	71.1	20	14 R45159
7	31	68.9	30	21 Y69503
8	30	66.7	20	20 W82295
9	30	66.7	23	20 W82310
10	29	64.4	15	11 Y17929
11	29	64.4	15	11 R34237
12	29	64.4	27	20 W78130

13	28	62.2	7	19	Y21365	Human HUPF-1 mutan
14	27 <td>60.0<td>9<td>16<td>R79676<td>Cyclin B/p3(cdc2)</td></td></td></td></td>	60.0 <td>9<td>16<td>R79676<td>Cyclin B/p3(cdc2)</td></td></td></td>	9 <td>16<td>R79676<td>Cyclin B/p3(cdc2)</td></td></td>	16 <td>R79676<td>Cyclin B/p3(cdc2)</td></td>	R79676 <td>Cyclin B/p3(cdc2)</td>	Cyclin B/p3(cdc2)
15	27 <td>60.0<td>9<td>17<td>W07056<td>Synthetic peptide</td></td></td></td></td>	60.0 <td>9<td>17<td>W07056<td>Synthetic peptide</td></td></td></td>	9 <td>17<td>W07056<td>Synthetic peptide</td></td></td>	17 <td>W07056<td>Synthetic peptide</td></td>	W07056 <td>Synthetic peptide</td>	Synthetic peptide
16	27 <td>60.0<td>9<td>19<td>W70120<td>Peptide produced b</td></td></td></td></td>	60.0 <td>9<td>19<td>W70120<td>Peptide produced b</td></td></td></td>	9 <td>19<td>W70120<td>Peptide produced b</td></td></td>	19 <td>W70120<td>Peptide produced b</td></td>	W70120 <td>Peptide produced b</td>	Peptide produced b
17	27 <td>60.0<td>9<td>21<td>V57975<td>Chicken lamin B2 p</td></td></td></td></td>	60.0 <td>9<td>21<td>V57975<td>Chicken lamin B2 p</td></td></td></td>	9 <td>21<td>V57975<td>Chicken lamin B2 p</td></td></td>	21 <td>V57975<td>Chicken lamin B2 p</td></td>	V57975 <td>Chicken lamin B2 p</td>	Chicken lamin B2 p
18	27 <td>60.0<td>11<td>19<td>W70126<td>Peptide produced b</td></td></td></td></td>	60.0 <td>11<td>19<td>W70126<td>Peptide produced b</td></td></td></td>	11 <td>19<td>W70126<td>Peptide produced b</td></td></td>	19 <td>W70126<td>Peptide produced b</td></td>	W70126 <td>Peptide produced b</td>	Peptide produced b
19	27 <td>60.0<td>16<td>15<td>R58353<td>Porcine parvovirus</td></td></td></td></td>	60.0 <td>16<td>15<td>R58353<td>Porcine parvovirus</td></td></td></td>	16 <td>15<td>R58353<td>Porcine parvovirus</td></td></td>	15 <td>R58353<td>Porcine parvovirus</td></td>	R58353 <td>Porcine parvovirus</td>	Porcine parvovirus
20	27 <td>60.0<td>25<td>16<td>R79982<td>Signal transductio</td></td></td></td></td>	60.0 <td>25<td>16<td>R79982<td>Signal transductio</td></td></td></td>	25 <td>16<td>R79982<td>Signal transductio</td></td></td>	16 <td>R79982<td>Signal transductio</td></td>	R79982 <td>Signal transductio</td>	Signal transductio
21	26 <td>57.8<td>19<td>19<td>W81232<td>Human eNOS peptide</td></td></td></td></td>	57.8 <td>19<td>19<td>W81232<td>Human eNOS peptide</td></td></td></td>	19 <td>19<td>W81232<td>Human eNOS peptide</td></td></td>	19 <td>W81232<td>Human eNOS peptide</td></td>	W81232 <td>Human eNOS peptide</td>	Human eNOS peptide
22	26 <td>57.8<td>19<td>19<td>W81332<td>Human iNOS peptide</td></td></td></td></td>	57.8 <td>19<td>19<td>W81332<td>Human iNOS peptide</td></td></td></td>	19 <td>19<td>W81332<td>Human iNOS peptide</td></td></td>	19 <td>W81332<td>Human iNOS peptide</td></td>	W81332 <td>Human iNOS peptide</td>	Human iNOS peptide
23	26 <td>57.8<td>21</td><td>14<td>R37992<td>Heavy chain hinge</td></td></td></td>	57.8 <td>21</td> <td>14<td>R37992<td>Heavy chain hinge</td></td></td>	21	14 <td>R37992<td>Heavy chain hinge</td></td>	R37992 <td>Heavy chain hinge</td>	Heavy chain hinge
24	26 <td>57.8<td>27<td>20<td>Y38474<td>Human secreted pro</td></td></td></td></td>	57.8 <td>27<td>20<td>Y38474<td>Human secreted pro</td></td></td></td>	27 <td>20<td>Y38474<td>Human secreted pro</td></td></td>	20 <td>Y38474<td>Human secreted pro</td></td>	Y38474 <td>Human secreted pro</td>	Human secreted pro
25	26 <td>57.8<td>28<td>20<td>Y03800<td>Murine LckBP1 pept</td></td></td></td></td>	57.8 <td>28<td>20<td>Y03800<td>Murine LckBP1 pept</td></td></td></td>	28 <td>20<td>Y03800<td>Murine LckBP1 pept</td></td></td>	20 <td>Y03800<td>Murine LckBP1 pept</td></td>	Y03800 <td>Murine LckBP1 pept</td>	Murine LckBP1 pept
26	25	55.6 <td>13<td>19<td>W71101<td>Amino-terminal pep</td></td></td></td>	13 <td>19<td>W71101<td>Amino-terminal pep</td></td></td>	19 <td>W71101<td>Amino-terminal pep</td></td>	W71101 <td>Amino-terminal pep</td>	Amino-terminal pep
27	25	55.6 <td>15<td>15<td>R46793<td>Phytase derived pe</td></td></td></td>	15 <td>15<td>R46793<td>Phytase derived pe</td></td></td>	15 <td>R46793<td>Phytase derived pe</td></td>	R46793 <td>Phytase derived pe</td>	Phytase derived pe
28	25	55.6 <td>17<td>19<td>W71102<td>Amino-terminal pep</td></td></td></td>	17 <td>19<td>W71102<td>Amino-terminal pep</td></td></td>	19 <td>W71102<td>Amino-terminal pep</td></td>	W71102 <td>Amino-terminal pep</td>	Amino-terminal pep
29	25	55.6 <td>18<td>19<td>W71105<td>Amino-terminal pep</td></td></td></td>	18 <td>19<td>W71105<td>Amino-terminal pep</td></td></td>	19 <td>W71105<td>Amino-terminal pep</td></td>	W71105 <td>Amino-terminal pep</td>	Amino-terminal pep
30	25	55.6 <td>18<td>21<td>Y65778<td>Protein tyrosine p</td></td></td></td>	18 <td>21<td>Y65778<td>Protein tyrosine p</td></td></td>	21 <td>Y65778<td>Protein tyrosine p</td></td>	Y65778 <td>Protein tyrosine p</td>	Protein tyrosine p
31	25	55.6 <td>19<td>21<td>Y65779<td>Protein tyrosine p</td></td></td></td>	19 <td>21<td>Y65779<td>Protein tyrosine p</td></td></td>	21 <td>Y65779<td>Protein tyrosine p</td></td>	Y65779 <td>Protein tyrosine p</td>	Protein tyrosine p
32	25	55.6 <td>20<td>14<td>R37689<td>Synthetic epitope.</td></td></td></td>	20 <td>14<td>R37689<td>Synthetic epitope.</td></td></td>	14 <td>R37689<td>Synthetic epitope.</td></td>	R37689 <td>Synthetic epitope.</td>	Synthetic epitope.
33	25	55.6 <td>20<td>15<td>R46816<td>Phytase derived pe</td></td></td></td>	20 <td>15<td>R46816<td>Phytase derived pe</td></td></td>	15 <td>R46816<td>Phytase derived pe</td></td>	R46816 <td>Phytase derived pe</td>	Phytase derived pe
34	25	55.6 <td>20<td>19<td>W71599<td>Protein tyrosine p</td></td></td></td>	20 <td>19<td>W71599<td>Protein tyrosine p</td></td></td>	19 <td>W71599<td>Protein tyrosine p</td></td>	W71599 <td>Protein tyrosine p</td>	Protein tyrosine p
35	25	55.6 <td>20<td>19<td>W71103<td>Amino-terminal pep</td></td></td></td>	20 <td>19<td>W71103<td>Amino-terminal pep</td></td></td>	19 <td>W71103<td>Amino-terminal pep</td></td>	W71103 <td>Amino-terminal pep</td>	Amino-terminal pep
36	25	55.6 <td>20<td>21<td>Y81933<td>Peptide fragment o</td></td></td></td>	20 <td>21<td>Y81933<td>Peptide fragment o</td></td></td>	21 <td>Y81933<td>Peptide fragment o</td></td>	Y81933 <td>Peptide fragment o</td>	Peptide fragment o
37	25	55.6 <td>22<td>13<td>R28278<td>Sequence of cowpea</td></td></td></td>	22 <td>13<td>R28278<td>Sequence of cowpea</td></td></td>	13 <td>R28278<td>Sequence of cowpea</td></td>	R28278 <td>Sequence of cowpea</td>	Sequence of cowpea
38	25	55.6 <td>24<td>19<td>Y20591<td>Human neurofilamen</td></td></td></td>	24 <td>19<td>Y20591<td>Human neurofilamen</td></td></td>	19 <td>Y20591<td>Human neurofilamen</td></td>	Y20591 <td>Human neurofilamen</td>	Human neurofilamen
39	25	55.6 <td>26<td>21<td>Y65782<td>Protein tyrosine p</td></td></td></td>	26 <td>21<td>Y65782<td>Protein tyrosine p</td></td></td>	21 <td>Y65782<td>Protein tyrosine p</td></td>	Y65782 <td>Protein tyrosine p</td>	Protein tyrosine p
40	25	55.6 <td>27<td>19<td>W71104<td>Amino-terminal pep</td></td></td></td>	27 <td>19<td>W71104<td>Amino-terminal pep</td></td></td>	19 <td>W71104<td>Amino-terminal pep</td></td>	W71104 <td>Amino-terminal pep</td>	Amino-terminal pep
41	25	55.6 <td>27<td>21<td>Y65783<td>Protein tyrosine p</td></td></td></td>	27 <td>21<td>Y65783<td>Protein tyrosine p</td></td></td>	21 <td>Y65783<td>Protein tyrosine p</td></td>	Y65783 <td>Protein tyrosine p</td>	Protein tyrosine p
42	25	55.6 <td>28<td>19<td>Y21018<td>Human gIIal fibril</td></td></td></td>	28 <td>19<td>Y21018<td>Human gIIal fibril</td></td></td>	19 <td>Y21018<td>Human gIIal fibril</td></td>	Y21018 <td>Human gIIal fibril</td>	Human gIIal fibril
43	24	53.3 <td>9</td> <td>14<td>R46520<td>HIV gag protein re</td></td></td>	9	14 <td>R46520<td>HIV gag protein re</td></td>	R46520 <td>HIV gag protein re</td>	HIV gag protein re
44	24	53.3 <td>10</td> <td>20<td>Y53419<td>HIV-1 p24 protein</td></td></td>	10	20 <td>Y53419<td>HIV-1 p24 protein</td></td>	Y53419 <td>HIV-1 p24 protein</td>	HIV-1 p24 protein
45	24	53.3 <td>10</td> <td>20<td>Y40268<td>Amino acid sequenc</td></td></td>	10	20 <td>Y40268<td>Amino acid sequenc</td></td>	Y40268 <td>Amino acid sequenc</td>	Amino acid sequenc

ALIGNMENTS

RESULT 1	R45168	standard; Protein; 9 AA.
XX	AC	R45168;
XX	DT	16-JUN-1994 (first entry)
XX	DE	Listeria p60 peptide epitope.
XX	KW	Listeria monocytogenes; antibodies; immunoassay; conjugate.
XX	OS	Synthetic.
PN	DE	DE4318450-A.
XX	PD	16-DEC-1993.
XX	PF	03-JUN-1993; 93DE-4318450.
XX	PR	11-JUN-1992; 92DE-4219111.
XX	PR	25-NOV-1992; 92DE-4239567.
XX	PA	(MERE) MERCK PATENT GMBH.
XX	PI	Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
XX	PI	Hofmann G, Buber A, Goebel W, Koehler S;
XX	DR	WPI: 1993-406956/51.
XX	PT	New primers for PCR detection of Listeria - including individual
XX	PT	species, also new peptide(s) for raising antibodies for
XX	PT	immunochemical detection
XX	PS	Disclosure: Flg 2; 19pp; German.

XX The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.

SQ Sequence 9 AA:

Query Match 100.0%; Score 45; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPQ 9
 |||||
 Db 1 vstpvapq 9

RESULT 2

R73891 R73891 standard; peptide; 21 AA.

XX R73891:

XX 05-DEC-1995 (first entry)

XX *Listeria* monocytogenes protein p60 precursor peptide 144-164.

XX *Listeria* monocytogenes; protein p60 precursor; vaccine;

KW meningitis related homologous antigenic sequence; MRNAS: RV-1;
 KM immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KM viral; peptide 144-164.

XX *Listeria* monocytogenes.

PN W09509232-A.

XX 06-APR-1995.

PF 28-SEP-1994; 94WO-CA00516.

PR 28-SEP-1993; 93US-0127499.

XX (SHAR/) SHARMA L. R.

PA (VALS/) VAN ALSTYNE D.

PI Sharma LR, Van Alstyne D;

XX WPI: 1995-147431/19.

XX New peptide(s) and corresp. antibodies for the treatment of

PT meningitis - the peptide(s) corresp. to homologous antigenic

XX sites on bacterial and viral agents and on chemokine(s), used for

XX detecting and preventing meningitis.

PS Claim 34; Page 74; 98pp; English.

XX R73913 is the *Listeria* monocytogenes protein p60 precursor. It

CC contains the meningitis related antigenic sequences (MRNAS) claimed

CC in R73891-R73894 and R73903-R73906, which are recognised by a

CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The

CC claimed MRNAS peptides may be used in immunoassays to diagnose the

CC presence of bacterial and/or viral meningitis agents in a sample,

CC or in prophylactic and therapeutic meningitis treatments. The

XX peptides may also be used as vaccines against meningitis.

SQ Sequence 21 AA:

Query Match 100.0%; Score 45; DB 16; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVAPQ 9
 |||||
 Db 2 vstpvapq 10

RESULT 3

R45172 R45172 standard; Protein; 12 AA.

XX R45172:

XX 16-JUN-1994 (first entry)

XX *Listeria* p60 peptide epitope.

XX *Listeria* monocytogenes; antibodies; immunoassay; conjugate.

OS Synthetic.

PN DE4318450-A.

XX 16-DEC-1993.

PF 03-JUN-1993; 93DE-4318450.

PR 11-JUN-1992; 92DE-421911.

PR 25-NOV-1992; 92DE-4239567.

XX (MERE) MERCK PATENT GMBH.

PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;

PI Hofmann G, Bubert A, Goebel W, Koehler S;

XX WPI: 1993-406956/51.

XX New primers for PCR detection of *Listeria* - including individual

PT species, also new peptide(s) for raising antibodies for

PT immunochemical detection

XX Disclosure; Fig 2; 19pp; German.

XX The sequence is that of a *Listeria* p60 peptide epitope which

CC which may be used in the prodn. of antibodies for the detection

CC of *Listeria* by immunoassay (partic. ELISA). It may be used as

CC part of a method that allows determination of individual *Listeria*

CC species, esp. *L. monocytogenes*.

XX Sequence 12 AA:

QY 2 STPVAPQ 9
 |||||
 Db 1 stpvapq 8

RESULT 4

R54615 R54615 standard; Protein; 6 AA.

XX R54615:

XX 16-JUN-1994 (first entry)

XX *Listeria* p60 peptide epitope.

XX *Listeria* monocytogenes; antibodies; immunoassay; conjugate.

OS Synthetic.

XX DE4318450-A.
 PN 16-DEC-1993.
 XX
 PD 03-JUN-1993; 93DE-4318450.
 XX
 PF 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure; Page 3; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 XX
 SQ Sequence 6 AA:

Query Match 71.1%; Score 32; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPRO 9
 |||||
 Db 1 pvaprq 6

RESULT 5
 R45173
 ID R45173 standard; Protein; 10 AA.
 XX
 AC R45173;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria p60 peptide epitope.
 XX
 KM Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for

PT immunochemical detection
 XX
 PS Disclosure; Fig 2; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 XX
 SQ Sequence 10 AA:

Query Match 71.1%; Score 32; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPRO 9
 |||||
 Db 1 pvaprq 6

RESULT 6
 R45159
 ID R45159 standard; Protein; 20 AA.
 XX
 AC R45159;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria p60 peptide epitope.
 XX
 KM Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 FH Key
 FT 1..7 Location/Qualifiers
 FT Region /note= "opt. 0-7 amino acid residues"
 FT 14..20
 FT Region /note= "opt. 0-7 amino acid residues"
 XX
 DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Claim 3; Page 4; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 XX
 SQ Sequence 20 AA:

Query Match 71.1%; Score 32; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVAPTO 9
 |||||
 Db 8 pvpapq 13

RESULT 7
 Y69503

ID Y69503 standard; peptide; 30 AA.

AC Y69503;

DT 10-APR-2000 (first entry)

XX C-terminalus of MMLV ecotropic env variant construct 2.

XX Envelope protein; env; gp70; ecotropic; MMLV; MCART1 receptor;

KM targeted delivery; gene therapy vehicle; retroviral; phage display;

XX mutant; mutain.

OS Moloney murine leukemia virus.

XX Synthetic.

PN EP972841-A1.

XX 19-JAN-2000.

XX 20-MAY-1999; 99EP-0201592.

XX 20-MAY-1998; 98EP-0201678.

XX (INTNR-) INTROGENE BV.

PI Van Es II;

DR WPI: 2000-099858/09.

XX New methods for producing gene transfer vehicles, useful for targeted

PT delivery of substances to cells -

PS Example 1; Page 17; 31pp; English.

XX This sequence represents the C-terminal sequence of a Moloney

CC murine leukemia virus (MMLV) gp70 envelope (env) protein mutant,

CC construct 2, used in an exemplification of the present invention.

CC The gp70 protein is one of two components of retroviral env proteins,

CC and is derived from the env gene-encoded precursor via proteolytic

CC cleavage. gp70 is responsible for binding a host cell-surface receptor,

CC thereby determining host range of the virus. MMLV is an ecotropic virus,

CC which binds to target cells via their MCART1 cationic amino acid

CC transporter. The invention relates to a method for selecting at least one

CC mutant viral protein (e.g., gp70) as a ligand capable of binding to a

CC cell-surface receptor. This method comprises displaying one or more

CC filamentous phage) and selecting the microorganism (e.g., a

CC bind to the cell-surface receptor. The invention also encompasses a

CC method for selecting for a filamentous phage expressing a protein capable

CC of binding to a ligand. The methods of the invention are used to select a

CC protein, or a filamentous phage displaying that protein, which is capable

CC of binding to a cell surface receptor. These methods may be used to

CC produce a virus-like particle or gene delivery vehicle which can be used

CC for gene transfer. This is useful for the targeted delivery of

CC substances to cells, such as nucleotides for use in gene therapy, or

CC compounds that kill tumour cells. The methods can be used to block the

CC productive infection of cells in a human patient, and mutant envelope

CC displaying phages that block a receptor can be used to treat pathogenic

CC virus infections. The methods are therefore especially useful for human

CC medicine. The gene transfer vehicles produced using the methods of the

CC invention enable better application of gene transfer therapy than prior

CC art methods. The prior art use of retroviruses are not highly effective

CC because all known env variants have a broad infection spectrum in
 CC common. The new methods modify the infection spectrum of virus-like
 CC particles, producing increased specificity and efficiency.

SO Sequence 30 AA;

Query Match 68.9%; Score 31; DB 21; Length 30;
 Best Local Similarity 71.4%; Pred. No. 35;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPTO 9
 ||::|||
 Db 4 tpisapq 10

RESULT 8
 W82295

ID W82295 standard; Peptide; 20 AA.

AC W82295;

DT 15-MAR-1999 (first entry)

XX Dynamin 41.20 ZELAN120 peptide.

XX Targeting agent; gastrointestinal tract; brain; drug delivery;

KM drug targeting; phage display; dynamin II, human.

XX Homo sapiens.

OS Synthetic.

XX Key

FM Modified-site

FM Location/Qualifiers

FM /note= "N-terminal danysyl group"

XX W09851825-A1.

XX 19-NOV-1998.

XX 15-MAY-1998; 98MO-US10079.

XX 15-MAY-1997; 97US-0857046.

XX (CYTO-) CYTOGEN CORP.

PA (ELAN-) ELAN CORP PLC.

XX Alvarez VL, O'Mahony DJ, Seveso M;

PI WPI: 1999-009778/01.

XX New targeting agents enabling transport of active agents through

PT human/animal tissue, or their uptake - useful in the treatment and

PT prevention of diseases, especially of the gastro-intestinal tract

PT (GIT)

XX Example 4; Page 53; 83pp; English.

XX This danylated peptide, termed dynamin 41.20 ZELAN120 peptide,

CC is a truncated fragment of dynamin 41.2 ZELAN086 peptide (see

CC W82294). Dynamin 41.2 is derived from human dynamin II and shows

CC homology to peptide 41.1 (see W82293), which was isolated from a

CC phage display library and shown to have the ability to enhance

CC transport of active agents from the gastrointestinal tract (GIT) to

CC brain. Dynamin 41.2 and peptide fragments of it (see W82295-97)

CC were compared with peptide 41.1 for their ability to enhance

CC transport of PLGA particles in vivo and in vitro. The invention

CC relates to targeting agents capable of permitting or facilitating

CC transport of an active agent through human or animal GIT tissue.

CC The targeting agents are peptides (see W82286-93), or their

CC derivatives (e.g. fragments, see W82300-10) and peptidomimetics,

CC and the nucleotide sequences coding for them (see V73312-19). They

CC have use in facilitating transport of active agents from the GIT

CC lumen into the systemic blood system and/or in targetting active
 CC agents to the GIT. Preferably, the active agent is a drug or
 CC drug-containing nanoparticle or microparticle.
 XX
 SQ Sequence 20 AA;

Query Match 66.7%; Score 30; DB 20; Length 20;
 Best Local Similarity 85.7%; Pred. NO. 34;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VSTPVAP 7
 |||||
 Db 5 vstpvpp 11

RESULT 9
 W82310
 ID W82310 standard; Peptide: 23 AA.

XX W82310;
 AC
 XX 15-MAR-1999 (first entry)
 DT
 XX Transport peptide fragment.
 DE

XX Targetting agent; gastrointestinal tract; brain; drug delivery;
 KM drug targetting; dynamini; human; transport peptide.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

PN WO9851825-A1.
 XX

PD 19-NOV-1998.
 XX

PF 15-MAY-1998; 98WO-US10079.
 XX

PR 15-MAY-1997; 97US-0857046.
 XX

PA (CYTO-) CYTOGEN CORP.
 (ELAN-) ELAN CORP PLC.
 XX

PI Alvarez VL, O'Mahony DJ, Seveso M;
 XX

DR WPI; 1999-009778/01.
 XX

XX New targetting agents enabling transport of active agents through
 PT human/animal tissue, or their uptake - useful in the treatment and
 PT prevention of diseases, especially of the gastro-intestinal tract
 (GIT)
 PT
 XX

PS Claim 10; Page 66; 83pp; English.
 XX

CC This is a fragment of dynamlin 41.2 (see W82294), a peptide derived
 CC from human dynamlin II. Claimed transport or uptake targetting
 CC agents can include this, or other, claimed peptide fragments (see
 CC W82300-10). Such transport or targetting agents permit or
 CC facilitate the transport of an active agent through a human or
 CC animal tissue such as gastrointestinal tract lumen, or uptake of
 CC the active agent into the human or animal tissue. The active agent
 CC is preferably a drug or drug-containing nanoparticle or
 CC microparticle. Therapeutic methods of administration,
 CC pharmaceutical compositions and formulations based of the
 CC targetting peptides are also provided.
 CC
 XX

XX Sequence 23 AA;
 SQ

Query Match 66.7%; Score 30; DB 20; Length 23;
 Best Local Similarity 85.7%; Pred. NO. 40;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VSTPVAP 7
 |||||
 Db 5 vstpvpp 11

RESULT 10
 Y17929
 ID Y17929 standard; peptide: 15 AA.
 XX
 AC Y17929;
 XX

DT 30-JUL-1999 (first entry)
 XX

XX Synthetic peptide derived from HTLV envelope sugar protein.
 DE

XX Hydrophilic peptide; antigen determinant; envelope sugar protein;
 KM HTLV-I; HTLV-II; B lymphatic corpuscle; gp46; gp63; tetanus toxoid.
 XX

XX Synthetic.
 OS Human lymphotropic virus type 1.
 OS
 XX

PN JP02209889-A.
 XX

PD 21-AUG-1990.
 XX

PF 08-FEB-1989; 89JP-0029551.
 XX

PR 30-JAN-1989; 89US-0303436.
 XX

PR 08-FEB-1988; 88US-0153420.
 XX

PA (UYDU-) UNIV DUKE.
 XX

DR WPI; 1990-344000/46.
 XX

PT Synthetic hydrophilic peptide - comprises 25 unit aminoacid that
 PT corresponds to at least one antigen determinant of envelope sugar
 PT protein(s) of HTLV-I and HTLV-II
 XX

PS Claim 5; Page 1; 15pp; Japanese.
 XX

CC The invention relates to new synthetic hydrophilic peptides (Y17922-934)
 CC that correspond to at least one of antigen determinants of envelope sugar
 CC proteins of HTLV-I and HTLV-II identified in the B lymphatic corpuscle.
 CC When bonded covalently to a carrier molecule, the peptides can induce the
 CC production of an antibody having a high titre to the gp46 and gp63
 CC envelope sugar proteins of HTLV-I and HTLV-II in mammals. The carrier
 CC molecule is preferably a tetanus toxoid and selected from the group of
 CC sequences shown in Y17935-39. The carrier molecule is preferably bonded
 CC to the peptide through at least one spacer molecule (preferably a
 CC dipeptide glycine-glycine). The peptides form effectively immunological
 CC response to factors causing virus HTLV-I and HTLV-II. The method also
 CC provides an effective conjugate having the peptide.
 CC
 XX

XX Sequence 15 AA;
 SQ

Query Match 64.4%; Score 29; DB 11; Length 15;
 Best Local Similarity 62.5%; Pred. NO. 38;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAPQ 9
 | : | : | : |
 Db 5 sspcsptq 12

RESULT 11
 R34237
 ID R34237 standard; peptide: 15 AA.
 XX

AC R34237;
 XX

DT 04-AUG-1993 (first entry)
 XX

DE HTLV-II envelope glycoprotein fragment 1.
XX Human T-cell leukemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies.
XX
OS Synthetic.
PN WO9306843-A.
XX
PD 15-APR-1993.
XX
PF 08-OCT-1992; 92MO-US08405.
XX
PR 08-OCT-1991; 91US-0771553.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI; 1993-134125/16.
XX
XX Antigenic determinant peptide(s) of HTLV envelope glyco:protein -
PT useful for detecting anti-HTLV-I and -II antibodies and as
PT vaccine against HTLV
XX
XX Claim 5; Page 13; 50pp; English.
XX
XX The sequence of peptide 1 corresponds to residues 30-44 from the
CC HTLV-II envelope glycoprotein. When covalently linked
CC to a carrier mol. the hydrophilic peptide can induce in a mammal the
CC prodn. of high titres of antibodies to gp46 envelope glycoprotein from
CC HTLV-I or -II. The peptide and carrier may be used in vaccines against
CC HTLV-I or -II infection. The peptide may be used in a diagnostic
CC assay to detect the presence and titre of anti-HTLV antibodies.
CC See also R34225-57.
XX
XX Sequence 15 AA:
SQ

Query Match 64.4%; Score 29; DB 14; Length 15;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 STPVAPRQ 9
I I I I I I
Db 5 sspcsptq 12

RESULT 12
W78130
ID W78130 standard; Protein: 27 AA.
XX
AC W78130;
XX
DT 13-APR-1999 (first entry)
XX
DE Human secreted protein encoded by gene 5 clone HPBDD36.
XX
KW Human: secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 27 /label= unknown
XX

PN WO9856804-A1.
XX
PD 17-DEC-1998.
XX
PF 11-JUN-1998; 98MO-US12125.
XX
PR 02-OCT-1997; 97US-0061060.
XX
PR 13-JUN-1997; 97US-0049547.
XX
PR 13-JUN-1997; 97US-0049548.
XX
PR 13-JUN-1997; 97US-0049549.
XX
PR 13-JUN-1997; 97US-0049550.
XX
PR 13-JUN-1997; 97US-0049606.
XX
PR 13-JUN-1997; 97US-0049607.
XX
PR 13-JUN-1997; 97US-0049608.
XX
PR 13-JUN-1997; 97US-0049609.
XX
PR 13-JUN-1997; 97US-0049610.
XX
PR 13-JUN-1997; 97US-0049611.
XX
PR 13-JUN-1997; 97US-0050366.
XX
PR 13-JUN-1997; 97US-0050901.
XX
PR 13-JUN-1997; 97US-0052989.
XX
PR 08-JUL-1997; 97US-0051919.
XX
PR 18-AUG-1997; 97US-0055984.
XX
PR 12-SEP-1997; 97US-0058665.
XX
PR 12-SEP-1997; 97US-0058668.
XX
PR 12-SEP-1997; 97US-0058669.
XX
PR 12-SEP-1997; 97US-0058750.
XX
PR 12-SEP-1997; 97US-0058971.
XX
PR 12-SEP-1997; 97US-0058972.
XX
PR 02-OCT-1997; 97US-0060834.
XX
PR 02-OCT-1997; 97US-0060841.
XX
PR 02-OCT-1997; 97US-0060844.
XX
PR 02-OCT-1997; 97US-0060865.
XX
PR 02-OCT-1997; 97US-0061059.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;
XX Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
XX Yu GL,
XX
DR WPI; 1999-080881/07.
XX
DR N-PSDB; X04315.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 11; Page 266; 380pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. X04302) for increasing the stability of the fused protein
CC as compared to the human protein only.
CC The invention relates to 86 novel genes and their fragments (nucleic acid
CC sequences: X04311-X04410; amino acid sequences W78126-W78225) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 86 polynucleotides, based on
CC which tissues they are most highly expressed in (see X04311 for described
XX uses).
XX
SQ Sequence 27 AA:
SQ

Query Match 64.4%; Score 29; DB 20; Length 27;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 PVAPRQ 9

Db 9 pvpaple 14

|||||:

RESULT 13

ID Y21365 standard. Protein: 7 AA.

XX Y21365;

AC Y21365;

XX Y21365;

PT 22-JUL-1999 (first entry)

XX Human HUPF-1 mutant protein fragment 17.

DE Human HUPF-1 precursor protein; beta-APP; diagnosis; cancer;

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;

KM frameshift mutation; age-related disease; neurodegenerative disorder;

KM Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;

KM Huntington's disease; multiple sclerosis; alcoholic liver disease;

KM diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;

KM ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;

KM neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;

KM glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;

KM bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMCP-C; MSP-A;

KM high mobility group protein-C; neuroendocrine specific protein A.

XX Synthetic.

OS Homo sapiens.

XX MO9845322-A2.

PN 15-OCT-1998.

PD 02-APR-1998; 98MO-IB00705.

XX 10-APR-1997; 97US-0043163.

PR (UYUT-) RIJKSUNIV UTRECHT.

XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX Burbach JPH, Grosveld FC, Van Leeuwen FW.

PI WPI; 1998-609901/51.

DR N-PSDB; X75768.

XX

PT Diagnosing disease by detecting frameshift mutations in RNA or

PT corresponding protein mutations - used to diagnose cancer and

PT neurological diseases, particularly Alzheimer's disease, and also

PT for treatment and prevention with specific ribozymes or wild-type

PT RNA

XX

PS Disclosure: Figure 17; 258bp; English.

XX

CC This invention describes a novel method for the diagnosis of a disease

CC caused by, or associated with, an RNA molecule that has a frameshift

CC mutation. The method is used to diagnose age-related diseases, especially

CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's

CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II

CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II

CC and many others listed) or susceptibility to these disorders. The method

CC allows a definitive diagnosis of Alzheimer's disease in living patients,

CC at an early stage. It is based on the observation that disease may be

CC caused by mutations in RNA rather than DNA. The invention describes the

CC use of neuronal system RNA molecules, specifically proteins including

CC beta-amyloid precursor protein (beta-APP), the microtubule associated

CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule

CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,

CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic

CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma

CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group

CC protein-C (HMCP-C) and neuroendocrine specific protein A.

XX

SO Sequence 7 AA:

Query Match 62.2%; Score 28; DB 19; Length 7;

Best Local Similarity 83.3%; Pred. No. 2.1e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 pvpaple 9

Db 2 pvpaple 7

|||||:

RESULT 14

ID R79676 standard; peptide; 9 AA.

XX R79676;

AC R79676;

XX 26-FEB-1996 (first entry)

DT Cyclin B/p33(cdc2) phosphorylation site in chicken lamin B2.

DE Cyclin B/p33(cdc2) phosphorylation site; protein kinase; substrate;

XX peptide library; competitor; cellular response; cell cycle control;

KW inhibitor; immune response; transcriptional activation; cell development.

KW Immune response; transcriptional activation; cell development.

XX Synthetic.

OS

XX MO9518823-A2.

PN 13-JUL-1995.

PD 06-JAN-1995; 95MO-US00147.

XX 07-JAN-1994; 94US-0178570.

PR (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX Cantley LC, Songyang Z;

PA WPI; 1995-255036/33.

DR

XX

PT Determination of amino acid sequence of protein kinase phosphorylation

PT site - by phosphorylation of peptide library and sequencing

PT phosphopeptide(s) formed, also new substrates and their analogues

PT for modulating or detecting protein kinase

XX

PS Example 6; Page 34; 131pp; English.

XX

CC An oriented degenerate peptide library of the amino acid formula

CC R79661 was constructed to isolate the amino acid sequences at the

CC phosphorylation sites of a protein kinase eg. protein kinase A.

CC cyclin B/p33(cdc2), src family kinases, etc. Peptides which are

CC phosphorylated are isolated and their amino acid sequences are compared

CC to known substrate/inhibitor peptide sequences for that protein kinase.

CC The peptides R79674-88 represent phosphorylation sites for the cell cycle

CC control kinases cyclin B/p33(cdc2) or cyclin B/p33(CDK2). This peptide

CC sequence is the phosphorylation site in the chicken lamin B2.

CC The isolated peptides can be used to screen cpts. for effects on the

CC protein kinase activity, generate antibodies to identify native kinase

CC substrates, or modulate a variety of cellular responses in which protein

CC kinases are involved eg. cell cycle control, immune response,

CC transcriptional activation or cell development.

XX

SO Sequence 9 AA:

Query Match 60.0%; Score 27; DB 16; Length 9;

Best Local Similarity 57.1%; Pred. No. 2.1e+05;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPQ 9

Db 2 TPVAPQ 8

|||||:

RESULT 15
W07056
XX W07056 standard; peptide; 9 AA.
XX
AC W07056;
XX
DT 21-JAN-1997 (first entry)
XX
DE Synthetic peptide used in GalNac-transferase activity SPA.
XX
DE Synthetic peptide used in GalNac-transferase activity SPA.
XX
KM SPA; scintillation proximity assay; antigen; bead coating; capture;
KM antibody; N-acetyl galactosamine transferase; GalNac transferase;
KW activity; enzyme; O-linked glycosylation.
XX
OS Synthetic.
XX
PN W09615258-A1.
XX
PD 23-MAY-1996.
XX
PF 08-NOV-1995; 95WO-US13483.
XX
PR 16-NOV-1994; 94US-0340283.
XX
PA (UPJO) UPJOHN CO.
XX
PI Elhammer AP;
XX
DR WPI: 1996-268220/27.
XX
PT Scintillation proximity assay for N-acetyl:galactosaminyl activity
PT - esp. for large scale screening of cpds. for their effect on enzyme
PT activity
XX
PS Claim 14; Page 17; 29pp; English.
XX
CC W06985-W07180 are antigenic peptides derived from either the
CC product of the human c-myc oncogene or the FLAG peptide (DYKDDDK).
CC The peptides are useful for coating beads used in a scintillation
CC proximity assay for N-acetylgalactosamine (GalNac)-transferase (GNT)
CC activity. The assay involves fewer steps than known assays and is
CC quicker, producing excellent signal-to-noise ratios. The
CC assay is capable of screening large numbers of cpds. for their
CC ability to affect GNT activity and is thus useful for identifying
CC inhibitors and promoters of glycosylation (in partic. O-linked
CC glycosylation).
XX
SQ Sequence 9 AA:

Query Match 60.0%; Score 27; DB 17; Length 9;
Best Local Similarity 83.3%; Pred. No. 2,1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 PVAPQ 9
11111
Db 1 pvlptg 6

Search completed: February 13, 2001, 13:02:01
Job time: 82 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:00:40 ; Search time 32.52 Seconds
(without alignments)
4.970 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 45

Sequence: 1 VSTPVAPNQ 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 111283

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/PCUS.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2	US-08-456-670B-26
2	45	100.0	21	1	US-08-127-499A-27
3	45	100.0	21	1	US-08-482-847-27
4	41	91.1	12	2	US-08-456-670B-30
5	32	71.1	10	2	US-08-456-670B-31
6	32	71.1	20	2	US-08-456-670B-17
7	29	64.4	15	1	US-08-116-733-15
8	27	60.0	9	1	US-08-178-570-29
9	27	60.0	9	2	US-08-340-283-81
10	27	60.0	9	3	US-08-369-643-29
11	27	60.0	9	4	PCT-US95-00147-29
12	27	60.0	16	1	US-08-307-724B-35
13	26	57.8	10	2	US-08-716-317-34
14	26	57.8	21	4	PCT-US97-10432-1
15	26	57.8	18	2	US-08-942-423-9
16	25	55.6	14	2	US-08-374-652C-12
17	25	55.6	14	2	US-08-374-652C-13
18	25	55.6	15	1	US-07-923-724-20
19	25	55.6	15	2	US-08-609-426A-20
20	25	55.6	20	1	US-07-923-724-43
21	25	55.6	20	2	US-08-609-426A-43
22	25	55.6	20	3	US-08-938-830-23
23	25	55.6	23	2	US-09-020-222-23
24	25	55.6	23	2	US-08-471-048-13
25	25	55.6	23	2	US-08-471-048-15
26	25	55.6	23	2	US-08-612-858-12
27	25	55.6	23	2	US-08-612-858-14
28	25	55.6	23	3	US-08-137-032-13

29	25	55.6	23	3	US-08-137-032-15	Sequence 15, Appl
30	25	55.6	24	2	US-08-374-652C-32	Sequence 32, Appl
31	24	53.3	9	1	US-08-146-145-24	Sequence 24, Appl
32	24	53.3	11	1	US-08-143-365A-4	Sequence 4, Appl
33	24	53.3	11	2	US-08-456-670B-29	Sequence 29, Appl
34	24	53.3	11	2	US-08-456-670B-38	Sequence 38, Appl
35	24	53.3	12	1	US-08-143-365A-5	Sequence 5, Appl
36	24	53.3	12	2	US-08-456-670B-42	Sequence 42, Appl
37	24	53.3	14	2	US-08-574-959A-12	Sequence 12, Appl
38	24	53.3	15	1	US-08-408-604A-31	Sequence 31, Appl
39	24	53.3	15	2	US-08-484-905-30	Sequence 30, Appl
40	24	53.3	15	3	US-08-481-985B-30	Sequence 30, Appl
41	24	53.3	15	3	US-08-370-476-30	Sequence 30, Appl
42	24	53.3	15	4	PCT-US93-09626-31	Sequence 31, Appl
43	24	53.3	18	2	US-09-017-205-24	Sequence 24, Appl
44	24	53.3	20	1	US-08-321-071A-18	Sequence 18, Appl
45	24	53.3	21	1	US-08-127-499A-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-456-670B-26
; Sequence 26, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINKEWILLER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: HUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P. C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456.670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-26

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
|||||
DB 1 VSTPVAPTQ 9

RESULT 2
US-08-127-499A-27
Sequence 27, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-27

Query Match 100.0%; Score 45; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
|||||
DB 2 VSTPVAPTQ 10

RESULT 3
US-08-482-847-27
Sequence 27, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-27

Query Match 100.0%; Score 45; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
|||||
DB 2 VSTPVAPTQ 10

RESULT 4
US-08-456-670B-30
Sequence 30, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWETTER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
LISTERIAS

```

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD

```

```

Query Match          99.1%; Score 41; DB 2; Length 12
Best Local Similarity 100.0%; Pred. NO. 0.13;
Matches:      8; Conservative 0; Mismatches 0; Indels 0

                2 STPVAPPTQ 9
                |||
                1 STPVAPPTQ 8

RESULT      5
US-08-456-670B-31
; Sequence 31, Application US/08456670B
; Patent NO. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, STEFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINKEWIELER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: HUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

```

```

TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 11-JUN-1993
APPLICATION NUMBER:
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/POCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

```

```

Query Match          71.1%; Score 32; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

OY      4 PVAPQ 9
          |||||
          1 PVAPQ 6

Db      1 PVAPQ 6

RESULT      6
US-08-456-6708-17
; Sequence 17 Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINKEWELER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BOBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN

```

```

; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: ECD
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1-7
; OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
; OTHER INFORMATION: MAY BE ABSENT"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14-20
; OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
; OTHER INFORMATION: MAY BE ABSENT"
; US-08-456-670B-17

Query Match      71.1%; Score 32; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PVAPQ 9
      111111
Db      8 PVAPQ 13

RESULT      7
US-08-116-733-15
; Sequence 15, Application US/08116733
```

```

; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-116-733-15

Query Match      64.4%; Score 29; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 STPVAPQ 9
      111111
Db      5 SPSQSPQ 12

RESULT      8
US-08-178-570-29
; Sequence 29, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song Yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
```


ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-178-570-29

Query Match 60.0%; Score 27; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAPTO 9
111111
Db 2 TPLSPTR 8

RESULT 9
US-08-340-283-81
Sequence 81, Application US/08340283
Patent No. 5861318
GENERAL INFORMATION:
APPLICANT: Elhammer, Ake P.
TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
TITLE OF INVENTION: N-ACETYLGLACTOSAMINYLTRANSFERASE ACTIVITY
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
ADDRESSSEE: (1920-32-1)
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,283
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Woolton, Thomas A.
REGISTRATION NUMBER: 35,004
REFERENCE/DOCKET NUMBER: 4828
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 385-7914
TELEFAX: (616) 385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-340-283-81

Query Match 60.0%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVAPTO 9
111111
Db 1 PVLPTQ 6

RESULT 10
US-08-369-643-29
Sequence 29, Application US/08369643A
Patent No. 6004757
GENERAL INFORMATION:
APPLICANT: Cantley, Lewis C.
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
FILE REFERENCE: CNS-001CP
CURRENT APPLICATION NUMBER: US/08/369,643A
CURRENT FILING DATE: 1995-01-06
EARLIER APPLICATION NUMBER: US 08/178,570
EARLIER FILING DATE: 1994-01-07
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chicken Iamln
US-08-369-643-29

Query Match 60.0%; Score 27; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVAPTO 9
111111
Db 2 TPLSPTR 8

RESULT 11
PCT-US95-00147-29
Sequence 29, Application PC/TUS9500147
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00147
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,570
FILING DATE: JANUARY 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-004CPPC
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
PCT-US95-00147-29

Query Match 60.0%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 TPVAPT 9
Db 2 TPVAPT 8

RESULT 12
US-08-307-724B-35
Sequence 35, Application US/08307724B
Patent No. 5785974
GENERAL INFORMATION:
APPLICANT: Jos Ignacio Casal Alvarez
APPLICANT: Carmen Vela Olmo
APPLICANT: Joannes Pieter Maria Langeveld
APPLICANT: Robert Hans Meleen
APPLICANT: Kristian Dalsgaard
TITLE OF INVENTION: "SYNTHETIC PEPTIDES AND
OPERATING SYSTEM: PC-DOS (version 3.30)
SOFTWARE: WordPerfect5.1 (WP5.1)
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: HARRISON & EGBERT
STREET: 1018 Preston Street, Suite 100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch., 1.2 MB storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS (version 3.30)
SOFTWARE: WordPerfect5.1 (WP5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,724B
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/ES94/00006
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: John S. Egbert
REGISTRATION NUMBER: 30627
REFERENCE/DOCKET NUMBER: 11553
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 223-4034
TELEFAX: (713) 223-4873
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: N-terminal end
ORIGINAL SOURCE:
ORGANISM: Porcine Parvovirus (PPV)
STRAIN: NADL-2
US-08-307-724B-35

Query Match 60.0%; Score 27; DB 1; Length 16;

Best Local Similarity 66.7%; Pred. No. 44;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 TPVAPT 8
Db 9 TPVAPT 14

RESULT 13
US-08-716-317-34
Sequence 34, Application US/08716317
Patent No. 5919634
GENERAL INFORMATION:
APPLICANT: HAMA, YUKO
APPLICANT: TOMODA, HIDEKI
APPLICANT: TSUKAMOTO, HIROKO
APPLICANT: NIKAIKO, KIYOKAZU
APPLICANT: KUNAGAI, HIROMICHI
TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
VECTOR CONTAINING IT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-317-34

Query Match 57.8%; Score 26; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 STPVAPT 8
Db 1 SAPVAPT 7

RESULT 14
PCT-US92-10432-1
Sequence 1, Application PC/RUS9210432

GENERAL INFORMATION:
APPLICANT: New England Medical Center
APPLICANT: Hospitals, Inc.
TITLE OF INVENTION: Infant Formula and Infant
TITLE OF INVENTION: Formula Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10432
FILING DATE: 19921203
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/802,338
FILING DATE: 04 December 1991
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/058W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US92-10432-1

Query Match 57.88; Score 26; DB 4; Length 21;
Best Local Similarity 62.58; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VSTPVAPT 8
| | | | |
Db 3 VSTPPTPS.10

RESULT 15
US-08-942-423-9
Sequence 9, Application US/08942423
Patent No. 5891673
GENERAL INFORMATION:
APPLICANT: Hashimoto, Yasuhiro
APPLICANT: Takemoto, Yoshihiro
TITLE OF INVENTION: Lock Binding Protein
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syntex (U.S.A.) Inc.
STREET: 3401 Hillview Ave.
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,423

FILING DATE: 01-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,715
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Perles, Rohan
REGISTRATION NUMBER: 35,752
REFERENCE/DOCKET NUMBER: 28260
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1698
TELEFAX: (415) 496-3529
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-942-423-9

Query Match 57.88; Score 26; DB 2; Length 28;
Best Local Similarity 55.68; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 VSTPVAPTQ 9
| | | | |
Db 12 VEEPAAPQ 20

Search completed: February 13, 2001, 13:03:16
Job time: 156 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:00:40 : Search time 35.7 Seconds
(without alignments)
17.118 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 45

Sequence: 1 VSTPVAPRTQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 6242

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_66:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	64.4	12	2 JU0356	cycloleucorin -
2	26	57.8	25	2 I40692	cena protein (IgA1)
3	26	57.8	30	2 A33308	thrombomodulin - r
4	24	53.3	18	2 A28027	protein P2 - curle
5	24	53.3	21	2 S32883	DNA gyrase chain A
6	24	53.3	24	2 A61505	pollen allergen Ph
7	23	51.1	14	2 A60158	disaggregatase - M
8	23	51.1	20	2 S38291	30k allergen - vel
9	23	51.1	23	2 F61491	seed protein ws-6
10	23	51.1	30	2 I40322	vir-repressed prot
11	22	48.9	16	2 PH1790	T cell receptor al
12	22	48.9	20	2 S72501	protein kinase C 1
13	22	48.9	20	2 B56385	nitrophorin 2 - Rh
14	22	48.9	24	2 S23121	1H-3-hydroxy-4-oxo
15	22	48.9	27	2 S09504	homeotic protein c
16	22	48.9	27	2 A49236	fibroblast-activat
17	22	48.9	30	2 S55462	me5 protein homol
18	21	46.7	15	2 S21242	H+-transporting AT
19	21	46.7	15	2 S28873	lipid transfer pro
20	21	46.7	16	2 A42411	myosin light chain
21	21	46.7	20	2 S33867	quinadilic acid 4-o
22	21	46.7	27	2 I51989	streptomycin 3''-a
23	21	46.7	28	2 I52394	fibronectin, splic
24	21	46.7	28	2 T37143	hypothetical prote
25	21	46.7	30	2 B60291	30k serine protein
26	20	44.4	8	2 S21288	lectin - potato (f
27	20	44.4	8	2 I54017	granulocyte-colony
28	20	44.4	12	2 PA0098	ribosomal protein
29	20	44.4	12	2 PD0021	muconate cycloisom

30	20	44.4	14	2 PH1806	T cell receptor al
31	20	44.4	15	2 S59492	formate dehydrogen
32	20	44.4	15	2 A40634	orf19 3' of eryk -
33	20	44.4	15	2 PS0455	superoxide dismuta
34	20	44.4	20	2 S38288	50k allergen - per
35	20	44.4	20	2 A25335	myosin-light-chain
36	20	44.4	23	2 S38738	lipid transfer pro
37	20	44.4	25	2 A30590	cytochrome enteroto
38	20	44.4	27	2 F39690	neural cell adhesi
39	20	44.4	29	2 C24536	alpha-amylase/tryr
40	20	44.4	30	2 PH0256	T-cell receptor Vb
41	20	44.4	30	2 PC4172	profilin - rat (fr
42	20	44.4	30	2 A82137	hypothetical prote
43	20	44.4	30	2 S59482	hydroxyproline-ric
44	19	42.2	10	2 JP0072	ribosomal protein
45	19	42.2	12	2 PQ0786	MDH dehydrogenase

ALIGNMENTS

RESULT 1
JU0356
cycloleucorin - sagebrush motherwort
C:Species: Leonurus artemisia (sagebrush motherwort)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JU0356
R:Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.
Chem. Pharm. Bull. 39, 712-715, 1991
A:Title: Cycloleucorin, a cyclic peptide from Leonuri fructus.
A:Reference number: JU0356; MUID:91300597
A:Accession: JU0356
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIN>

Query Match Best Local Similarity 64.4%; Score 29; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TPVAPRTQ 9
DB 2 TPVAPRTQ 8

RESULT 2
I40692
cena protein (IgA1) - Cellulomonas fimi (fragment)
C:Species: Cellulomonas fimi
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C:Accession: I40692
R:Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; War
FEMS Microbiol. Lett. 92, 199-204, 1992
A:Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human
hoecae.
A:Reference number: I40692
A:Accession: I40692
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-25 <RES>
A:Cross-references: EMBL:X65780; NID:G312035; PIDN:CAA46663.1; PID:G312036

Query Match Best Local Similarity 57.8%; Score 26; DB 2; Length 25;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VSTPVAPT 8
DB 3 VSTPVAPT 10

```
RESULT 3
A33308
thrombomodulin - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 03-May-1996
C:Accession: A33308
R:Stearns, D.J.; Kurosawa, S.; Esmon, C.T.
J. Biol. Chem. 264, 3352-3356, 1989
A:Title: Microthrombomodulin. Residues 310-486 from the epidermal growth factor precursor
A:Reference number: A33308; MUID:9123461
A:Accession: A33308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-30 <STE>
C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology

Query Match 57.8%; Score 26; DB 2; Length 30;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 STPVAPPTQ 9
||| |||
Db 20 VSTECPTQ 28

RESULT 4
A28027
protein p2 - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C:Accession: A28027
R:Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A:Reference number: A94167
A:Accession: A28027
A:Molecule type: protein
A:Residues: 1-18 <BAU>
A>Note: 14-Arg was also found

Query Match 53.3%; Score 24; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PVAPPTQ 9
||| |
Db 10 PIAFGQ 15

RESULT 5
S32883
DNA gyrase chain A - Streptomyces spheroides (fragment)
C:Species: Streptomyces spheroides
C>Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 22-Oct-1999
C:Accession: S32883; S29684
R:Thiara, A.S.; Cundliffe, E.
Mol. Microbiol. 8, 495-506, 1993
A:Title: Expression and analysis of two gyrB genes from the novobiocin producer, Strept-
A:Reference number: S32881; MUID:93316846
A:Accession: S32883
A:Molecule type: DNA
A:Residues: 1-21 <THI>
A:Cross-references: EMBL:Z17305; NID:g47535; PIDN:CA78953.1; PID:g47537

Query Match 53.3%; Score 24; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 STPVAPPTQ 9
||||| |
Db 2 STPVAPPTQ 9

Query Match 53.3%; Score 24; DB 2; Length 24;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
||| |
Db 7 ATPAP 12

RESULT 6
A61505
pollen allergen Phl p V - common timothy (fragment)
C:Species: Phleum pratense (common timothy)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 07-May-1999
C:Accession: A61505
R:Mathiesen, F.; Lowenstein, H.
Clin. Exp. Allergy 21, 297-307, 1991
A:Title: Group V allergens in grass pollens. I. Purification and characterization of
A:Reference number: A61505; MUID:9132736
A:Accession: A61505
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-24 <MAT>
A>Note: 2-Ala, 5-Gly, and 15-Glu were also found
C:Superfamily: grass pollen allergen IX
C:Keywords: hydroxyproline; pollen
F:6,9,12,18,21,24/Modified site: hydroxyproline (Pro) #status experimental.

Query Match 53.3%; Score 24; DB 2; Length 24;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
||| |
Db 7 ATPAP 12

RESULT 7
A60158
disaggregatase - Methanosarcina mazei (strain LXC) (fragment)
C:Species: Methanosarcina mazei
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 07-May-1999
C:Accession: A60158
R:Xun, L.; Mah, R.A.; Boone, D.R.
Appl. Environ. Microbiol. 56, 3693-3698, 1990
A:Title: Isolation and characterization of disaggregatase from Methanosarcina mazei L
A:Reference number: A60158; MUID:91189693
A:Accession: A60158
A:Molecule type: protein
A:Residues: 1-14 <XUN>
C:Comment: Disaggregatase can release individual cells by hydrolyzing the characteris-

Query Match 51.1%; Score 23; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 TPVAP 7
||| |
Db 2 TPVAP 6

RESULT 8
S38291
30K allergen - velvet grass (fragment)
C:Species: Holcus lanatus (velvet grass)
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 19-May-2000
C:Accession: S38291
R:Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
A:Title: Comparison of four grass pollen species concerning their allergens of grass
A:Reference number: S38288; MUID:94092339
A:Accession: S38291
A:Molecule type: protein
A:Residues: 1-20 <PET>

Query Match 51.1%; Score 23; DB 2; Length 20;
```

Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0;
OY 3 TPVAP 7
1111
Db 6 TPVAP 10

RESULT 9
F61491
seed protein ws-6 - winged bean (fragment)
C:Species: Psophocarpus tetragonolobus (winged bean)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 03-May-1996
C:Accession: F61491
R:Hitano, H.
J. Protein Chem. 8, 115-130, 1989
A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gels
A:Reference number: A61491; MUID:89351606
A:Accession: F61491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <HIR>
C:Superfamily: pathogenesis-related protein
C:Keywords: seed

Query Match 51.1%; Score 23; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
1111
Db 10 TPVAP 15

RESULT 10
140322
viral-repressed protein - Bordetella pertussis (fragment)
C:Species: Bordetella pertussis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999
C:Accession: 140322
R:Beattie, D.T.; Mahan, M.J.; Mekalanos, J.J.
J. Bacteriol. 175, 519-527, 1993
A:Title: Repressor binding to a regulatory site in the DNA coding sequence is sufficient
A:Reference number: 140320; MUID:93123171
A:Accession: 140322
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-30 <RES>
A:Cross-references: GB:106123; NID:g144086; PIDN:AAA22989.1; PID:g551757
C:Genetics:
A:Gene: virg-73

Query Match 51.1%; Score 23; DB 2; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VSTPVA 6
1111
Db 9 VOTPIA 14

RESULT 11
PH1790
T cell receptor alpha chain V region (clone 2PBL V alpha 24-6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1790
R:Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585
A:Accession: PH1790
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR>

Query Match 48.9%; Score 22; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PVAPT 8
1111
Db 8 PITPT 12

RESULT 12
S72501
protein kinase C inhibitor - human (fragment)
N:Alternate names: histidine triad nucleotide-binding protein
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S72501; S62623
R:Maines, M.D.; Trakshel, G.M.
Arch. Biochem. Biophys. 300, 320-326, 1993
A:Title: Purification and characterization of human biliverdin reductase.
A:Reference number: S29736; MUID:93143333
A:Accession: S72501
A:Molecule type: protein
A:Residues: 1-20 <MAI>
A:Note: this protein was identified as biliverdin reductase; the identification is questionable
R:Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Eur. J. Biochem. 235, 372-381, 1996
A:Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterization
A:Reference number: S62622; MUID:96202961
A:Accession: S62623
A:Molecule type: protein
A:Residues: 1-20 <MAW>
C:Superfamily: protein kinase C inhibitor; histidine triad homology
C:Keywords: homodimer; protein kinase inhibitor; zinc

Query Match 48.9%; Score 22; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 TPVAPT 8
1111
Db 8 SPOAPT 13

RESULT 13
B56385
nitrophenol 2 - Rhodnius prolixus (fragment)
N:Alternate names: nitric oxide-carry protein NP2
C:Species: Rhodnius prolixus
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C:Accession: B56385
R:Champagne, D.E.; Nussenzveig, R.H.; Ribeiro, J.M.C.
J. Biol. Chem. 270, 8691-8695, 1995
A:Title: Purification, partial characterization, and cloning of nitric oxide-carrying
A:Reference number: A56385; MUID:95238361
A:Accession: B56385
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <CHA>
C:Keywords: heme; salivary gland; vasodilator

Query Match 48.9%; Score 22; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 STPVAPTQ 9
 || : | |
 Db 3 STNISPKQ 10

RESULT 14

S23121
 1H-3-hydroxy-4-oxoquinoline oxygenase - Pseudomonas putida
 C:Species: Pseudomonas putida
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C:Accession: S23121
 R:Block, D.W.; Lingsens, F.
 Biol. Chem. Hoppe-Seyler 373, 343-349, 1992
 A:title: Microbial metabolism of quinoline and related compounds. XIV. Purification and
 rain 33/1.
 A:Reference number: S23121; WUID:92384934
 A:Accession: S23121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-24 <BLO>

Query Match 48.9%; Score 22; DB 2; Length 24;
 Best Local Similarity 80.0%; Pred. NO. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 PVAPT 8
 | | | |
 Db 19 PXAPT 23

RESULT 15

S09504
 homeotic protein ceh-12 - Caenorhabditis elegans (fragment)
 C:Species: Caenorhabditis elegans
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 24-Sep-1999
 C:Accession: S09504
 R:Schaller, D.; Wiltmann, C.; Spicher, A.; Mueller, F.; Tobler, H.
 Nucleic Acids Res. 18, 2033-2036, 1990
 A:title: Cloning and analysis of three new homeobox genes from the nematode Caenorhabditis
 A:Reference number: S09503; WUID:90245646
 A:Accession: S09504
 A:Molecule type: DNA
 A:Residues: 1-27 <SCH>
 A:Cross-references: EMBL:X17076; NID:g6666; PIDN:CAA34928.1; PID:e20767; PID:g1335612.
 C:Genetics:
 A:Gene: ceh-12
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:1-14/Domain: homeobox homology (fragment) <HOX>

Query Match 48.9%; Score 22; DB 2; Length 27;
 Best Local Similarity 57.1%; Pred. No. 5.3e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 STPVAPT 8
 | | | |
 Db 18 STPIQST 24

Search completed: February 13, 2001, 13:02:40
 Job time: 120 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:02:08 ; Search time 20.83 Seconds

(without alignments)
13.953 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 45

Sequence: 1 STPVAPPTQ 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1785

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SWISSPROT_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	53.3	21	1	GYRA_STRSH
2	23	51.1	27	1	IPPD_MOUSE
3	22	48.9	27	1	HMI2_GAEU
4	21	46.7	15	1	ATP2_SPIOL
5	20	44.4	27	1	PAS5_CAPI
6	19	42.2	21	1	CHIC_PEA
7	19	42.2	24	1	ALKB_SALTY
8	19	42.2	29	1	HOXY_NOCOP
9	18	40.0	15	1	UCO8_MAIZE
10	18	40.0	19	1	TCBI_TRILO
11	18	40.0	21	1	LPT_ECOLI
12	18	40.0	23	1	IBP2_PIG
13	18	40.0	24	1	MDH_PLAVE
14	18	40.0	24	1	MDH_STRNS
15	17	37.8	12	1	TM2A_METMA
16	17	37.8	13	1	UNO2_PINS
17	17	37.8	17	1	A45K_MYCBO
18	17	37.8	19	1	AL17_OLFEU
19	17	37.8	19	1	COOT_SARBU
20	17	37.8	19	1	PHSL_DESBN
21	17	37.8	20	1	MDH_KIBAR
22	17	37.8	20	1	PSAL_SYNVU
23	17	37.8	24	1	BRIA_RANES
24	17	37.8	25	1	BOTR_BOTJA
25	17	37.8	25	1	RS19_ACHLA
26	17	37.8	27	1	LS2_ADE07
27	17	37.8	27	1	NIFD_MERIV
28	17	37.8	28	1	RS19_PHYS1
29	17	37.8	30	1	Y16P_BPT4
30	17	37.8	30	1	PAHX_RAT
31	16	35.6	9	1	DCML_PSRCF
32	16	35.6	9	1	TKC1_CALVO
33	16	35.6	10	1	AL19_CARMA

34	16	35.6	11	1	BPP_AGRHP	P04562 agk1strodon
35	16	35.6	11	1	D3H1_HUMAN	P31937 homo sapien
36	16	35.6	12	1	FARI_CALVO	P41869 calliphora
37	16	35.6	12	1	TAL0_TREME	P01371 tremella me
38	16	35.6	15	1	UC17_MAIZE	P80623 zea mays (m
39	16	35.6	15	1	UC30_MAIZE	P80636 zea mays (m
40	16	35.6	15	1	UE15_HORVU	P34938 hordeum vul
41	16	35.6	17	1	RM35_YEAST	P36530 saccharomyc
42	16	35.6	18	1	AGI_EUPCH	P33888 euphorbia c
43	16	35.6	19	1	DHAB_COMTE	P80704 comamonas t
44	16	35.6	20	1	CRP_MUSCA	P19094 mustelus ca
45	16	35.6	20	1	FRHA_METBA	P80489 methanosarc

ALIGNMENTS

RESULT	ID	GYRA_STRSH	STANDARD:	PRT:	21 AA.
AC	P50071				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	01-OCT-1996	(Rel. 34, Last annotation update)			
DE	DNA GYRASE SUBUNIT A (EC 5.99.1.3) (FRAGMENT).				
GN	GYRA.				
OS	Streptomyces spheeroides.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
CC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-NCIB 11891;				
RX	MEDLIN-93316846; PubMed-8392138;				
RA	Thiara A.S., Cundliffe E.:				
RT	"Expression and analysis of two gyrB genes from the novobiocin				
RT	producer, Streptomyces spheeroides.";				
RL	Mol. Microbiol. 8:495-506(1993).				
CC	-1- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-				
CC	STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE				
CC	INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED				
CC	DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.				
CC	-1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE AND REJOINING				
CC	OF DOUBLE-STRANDED DNA.				
CC	-1- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA				
CC	BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE				
CC	ENZYME FORMS AN A2B2 TETRAMER.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; 217305; CAA78953.1; -				
KW	Topoisomerase; Isomerase; DNA-binding.				
FT	NON_TER 21				
SO	SEQUENCE 21 AA; 2203 MW; 5E2P9DEA8DB83697 CRC64;				
Query Match					
Best Local Similarity 53.3%; Score 24; DB 1; Length 21;					
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;					
QY	2	STPVAPPTQ 9			
DB	5	NTVPAPPEE 12			
RESULT 2					
ID	IPPD_MOUSE	STANDARD:	PRT:	27 AA.	

AC 060829;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DOPAMINE- AND CAMP-REGULATED NEURONAL PHOSPHOPROTEIN (DARPP-32)
DE (FRAGMENT).
GN PPP1R1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C.
RX MEDLINE-96043524; PubMed-7485543;
RA Blau S., Daly L., Fienberg A., Teitelman G., Ehrlich M.E.;
RT "DARPP-32 promoter directs transgene expression to renal thick
ascending limb of loop of Henle."
RL Am. J. Physiol. 269:F564-F570(1995)
CC -1- FUNCTION: INHIBITOR OF PROTEIN-PHOSPHATASE 1.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- PTM: DOPAMINE- AND CYCLIC AMP-REGULATED NEURONAL PHOSPHOPROTEIN
(BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PHOSPHATASE INHIBITOR 1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U23160; AAA93223.1; -
DR Protein phosphatase inhibitor; Acetylation.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 3139 MW; 2FCB2C85F9458444 CRC64;

Query Match 51.1%; Score 23; DB 1; Length 27;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 STPVAPTQ 9
ID 1 1 1
DB 12 SVDPAPSQ 19

RESULT 3
HM12_CAEEL STANDARD; PRT; 27 AA.
AC P17487;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HOMEBOX PROTEIN CEH-12 (FRAGMENT).
GN CEH-12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90245646; PubMed-1970877;
RA Schaller D., Wiltmann C., Spicher A., Mueller F., Tobler H.;
RT "Cloning and analysis of three new homeobox genes from the nematode
RT Caenorhabditis elegans."
RL Nucleic Acids Res. 18:2033-2036(1990).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X17076; CAA34928.1; -
DR PIR: S09504; S09504.
DR HSSP: P02833; IHOM.
DR INTERPRO: IPR001356; -
DR PFAM: PF00046; homeobox; 1.
DR PROSITE: PS00027; HOMEBOX_1; PARTIAL.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND <1 16 HOMEBOX.
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 3182 MW; FDAFD5D16F3870A5 CRC64;

Query Match 48.9%; Score 22; DB 1; Length 27;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 STPVAPT 8
ID 1 1 1
DB 18 STPIQST 24

RESULT 4
ATP2_SPIOL STANDARD; PRT; 15 AA.
ID ATP2_SPIOL
AC P80083;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).
GN ATPB OR ATP2.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC Caryophyllales; Chenopodiaceae; Spinacia.
RN [1]
RP SEQUENCE.
RC STRAIN-CV. MEDANIA; TISSUE-LEAF MESOPHYLL;
RX MEDLINE-92209531; PubMed-1313368;
RA Hamasur B., Glaser E.;
RT "Plant mitochondrial F0F1 ATP synthase. Identification of the
RT individual subunits and properties of the purified spinach leaf
RT mitochondrial ATP synthase."
RL Eur. J. Biochem. 205:409-416(1992).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
DR PIR: S21242; S21242.
DR INTERPRO: IPR000194; -
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KM ATP synthase; CF(1); Hydrogen ion transport;
KM Hydrolyase; ATP-binding; Mitochondrion.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1295 MW; E5826224F63EE2CF CRC64;

Query Match 46.7%; Score 21; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 STPVYA 6
ID 1 1 1

Db 11 STPLA 15

RESULT 5
PAS5_CAPHI STANDARD; PRT: 27 AA.

AC P80935;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PREGNANCY-ASSOCIATED GLYCOPROTEIN 55 (EC 3.4.23.-) (PAG 55)
DN (FRAGMENT).
GN PAG55.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
RN [1]
RP SEQUENCE.
RC TISSUE=PLACENTA;
RX MEDLINE=98132272; Pubmed=9472930;
RA Garbayo J.M., Remy B., Alabart J.L., Folch J., Mattiez R.,
RA Falmagne P., Beckers J.F.,
RT "Isolation and partial characterization of a pregnancy-associated
glycoprotein family from the goat placenta."
RL Biol. Reprod. 58:109-115(1998).
CC -1- TISSUE SPECIFICITY: PLACENTA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE
EUKARYOTIC ASPARTYL PROTEASES FAMILY.
DR INTERPRO: IPR001969; -
DR PROSITE: PS00141; ASP_PROTEASE; PARTIAL.
KW Hydrolase; Aspartyl protease; Glycoprotein.
FT NON_TER 27
SQ SEQUENCE 27 AA; 3005 MW; 056180578F4AF625 CRC64;

Query Match 44.4%; Score 20; DB 1; Length 27;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSTPVA 6
: : : : :
: : : : :
Db 1 ISSPVS 6

RESULT 6
CHIC_PEA STANDARD; PRT: 21 AA.

ID CHIC_PEA
AC P31233;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 10 KDA CHAPERONIN, CHLOROPLAST (PROTEIN CPN10) (PROTEIN GROES)
(FRAGMENT).
GN CPN10.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
RN [1]
RP SEQUENCE.
RX MEDLINE=92409583; Pubmed=1356267;
RA Bertsch U., Soll J., Seetharam R., Viltanen P.V.,
RT "Identification, characterization, and DNA sequence of a functional
'double' groes-like chaperonin from chloroplasts of higher plants."
Proc. Natl. Acad. Sci. U.S.A. 89:8696-8700(1992).
CC -1- FUNCTION: SEEMS TO FUNCTION ONLY AS A COCHAPERONIN, ALONG WITH
CPN60, AND IN CERTAIN CASES IS ESSENTIAL FOR THE DISCHARGE OF
BIOLOGICALLY ACTIVE PROTEINS FROM CPN60.
CC -1- SUBUNIT: FORMS STABLE COMPLEXES WITH CPN60 IN THE PRESENCE
OF ATP.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.

DR INTERPRO: IPR001476; -
DR PFAM: PF00166; CPN10; 1.
DR PROSITE: PS00681; CHAPERONINS_CPN10; PARTIAL.
KW Chaperone; Chloroplast.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2240 MW; 260295B3C087ED95 CRC64;

Query Match 42.2%; Score 19; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 STPVAP 7
: : : : :
: : : : :
Db 1 ATPVAP 6

RESULT 7
ALKB_SALTY STANDARD; PRT: 24 AA.

ID ALKB_SALTY
AC P37462;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ALKYLATED DNA REPAIR PROTEIN ALKB (FRAGMENT).
GN ALKB.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91267928; Pubmed=1904855;
RA Hakura A., Morimoto K., Sofuni T., Nohmi T.;
RT "Cloning and characterization of the Salmonella typhimurium ada gene,
which encodes O6-methylguanine-DNA methyltransferase."
RL J. Bacteriol. 173:3663-3672(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE REPAIR OF ALKYLATED DNA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90221; -; NOT_ANNOTATED_CDS.
DR PIR: B39433;
DR STYGENE; SG10006; ALKB.
KW DNA repair.
FT NON_TER 24
SQ SEQUENCE 24 AA; 2780 MW; CBB948C28FF908F3 CRC64;

Query Match 42.2%; Score 19; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FVAP 7
: : : : :
: : : : :
Db 14 PLAP 17

RESULT 8
HOXY_NOCOP STANDARD; PRT: 29 AA.

ID HOXY_NOCOP
AC P22660;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NAD-REDUCING HYDROGENASE HOXS DELTA SUBUNIT (EC 1.1.2.1.2) (FRAGMENT).
GN HOXY.
OS Nocardia opaca.

OC Plasmid.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-1B;
 RX MEDLINE-89231684; PubMed-2496982;
 RA Zaborosch C., Schneider K., Schlegel H.G., Kratzin H.;
 RT "Comparison of the NH₂-terminal amino acid sequences of the four non-
 identical subunits of the NAD-linked hydogenases from Nocardia opaca
 1b and Alcaligenes eutrophus H16."
 RL Eur. J. Biochem. 181:175-180(1989).
 CC -1- CATALYTIC ACTIVITY: H(2) + NAD(+) - H(+) + NADH.
 CC -1- COFACTOR: FMN, NICKEL, TWO 4FE-4S, A 3FE-4S, AND A 2FE-2S
 CC CLUSTER.
 CC -1- SUBUNIT: TETRAMER OF AN ALPHA AND A GAMMA SUBUNITS (FLAVIN-
 CONTAINING DIMER), AND A DELTA AND A NICKEL-CONTAINING BETA
 CC SUBUNITS (HYDROGENASE DIMER).
 CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC.
 CC -1- SIMILARITY: TO OTHER [NIFE] OR [NIFESE] HYDROGENASES SMALL
 CC SUBUNIT.
 DR PIR: S03947; S03947.
 DR Oxidoreductase; NAD; Iron-sulfur; 3Fe-4S; Plasmid.
 FT NON_TER 29
 FT SEQUENCE 29 AA; 3159 MW; 1F54BC68F66AD6A CRC64;
 SQ

Query Match 42.2%; Score 19; DB 1; Length 29;
 Best Local Similarity 50.0%; Pred. No. 1e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 STVPAP 7
 DB 16 TTPLDP 21

RESULT 9
 UC08_MAIZE STANDARD; PRT; 15 AA.
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
 DE (FRAGMENT).
 DE Zea mays (Maize).
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-COLEOPTILE;
 RA Touzet P., Riccardi F., Morin C., Damerival C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 38.8 KDA.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR MAIZE2DPAGE: P80614; COLEOPTILE.
 DR MAIZEDB: 123934; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 FT SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4D0F8D CRC64;
 SQ

Query Match 40.0%; Score 18; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 7.9e+02;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 4 PVAP 7
 DB 11 1

DB 9 PVAP 12
 RESULT 10
 TCBL_TRILIO STANDARD; PRT; 19 AA.
 ID TCBL_TRILIO
 AC P80070;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TRICHOLOMGIN BI AND BII.
 OS Trichoderma longibrachiatum.
 OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Trichoderma.
 RN [1]
 RP SEQUENCE, AND STRUCTURE BY NMR.
 RX MEDLINE-92037622; PubMed-1935961;
 RA Reduffat S., Prigent Y., Auvin-Guette C., Bodo B.;
 RT "Tricholongins BI and BII, 19-residue pepatolols from Trichoderma
 RT longibrachiatum. Solution structure from two-dimensional NMR
 RT spectroscopy."
 RL Eur. J. Biochem. 201:661-674(1991).
 CC -1- FUNCTION: TRICHOLOMGINS ARE PEPTIDES WHICH DISPLAY ANTIFUNGAL
 CC AND ANTIBACTERIAL ACTIVITY. PROBABLY INTERACT WITH BIOLOGICAL
 CC MEMBRANES AND PROBABLY PRODUCES HOLES LEADING TO LEAKAGE.
 CC -1- PTM: AIB IS ALPHA-AMINO ISOBUTYRIC ACID.
 CC -1- PTM: IVA IS ISOVALINE.
 CC Antibiotic; Fungicide; Methylation; Hydroxylation;
 KW Membrane.
 FT MOD_RES 1 1 ACETYLATION (TO FORM AIB).
 FT MOD_RES 1 1 METHYLATION (TO FORM AIB).
 FT MOD_RES 4 4 METHYLATION (TO FORM AIB).
 FT MOD_RES 5 5 METHYLATION (TO FORM AIB).
 FT MOD_RES 7 7 METHYLATION (TO FORM AIB).
 FT MOD_RES 8 8 METHYLATION (TO FORM AIB).
 FT MOD_RES 9 9 METHYLATION (TO FORM AIB).
 FT MOD_RES 12 12 METHYLATION (TO FORM AIB).
 FT MOD_RES 15 15 METHYLATION (TO FORM AIB).
 FT MOD_RES 16 16 METHYLATION (TO FORM AIB; IN BI).
 FT MOD_RES 16 16 ETHYLATION (TO FORM IVA; IN BII).
 FT MOD_RES 19 19 HYDROXYLATION.
 SQ SEQUENCE 19 AA; 1756 MW; B908C2DFE83D238 CRC64;
 DB

Query Match 40.0%; Score 18; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PVAP 9
 DB 13 PVAAQ 18

RESULT 11
 LPT_ECOLI STANDARD; PRT; 21 AA.
 ID LPT_ECOLI
 AC P03059;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE THR OPERON LEADER PEPTIDE (THR OPERON ATTENUATOR).
 GN THRL.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-79201669; PubMed-287010;
 RA Gardner J.F.;
 RT "regulation of the theonine operon: tandem threonine and isoleucine
 RT codons in the control region and translational control of
 RT transcription termination."
 RL Proc. Natl. Acad. Sci. U.S.A. 76:1706-1710(1979).
 DB [2]

RP SEQUENCE FROM N.A.
 RA MEDLINE-85264808; PubMed-2410621;
 RX Lynn S.P., Bauer C.E., Chapman K.A., Gardner J.F.;
 RT "Identification and characterization of mutants affecting
 transcription termination at the threonine operon attenuator.";
 RL J. Mol. Biol. 183:529-541(1985).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-95334362; PubMed-7610040;
 RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
 region from 92.8 through 100 minutes.";
 RL Nucleic Acids Res. 23:2105-2119(1995).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 OF THREONINE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: V00360; CAA23658.1; -
 DR EMBL: X68872; CAA4873.1; -
 DR EMBL: J01706; AAA83913.1; -
 DR EMBL: M28570; AAA24672.1; -
 DR EMBL: U14003; AAA97300.1; -
 DR EMBL: AE000111; AAC73112.1; -
 DR PIR: A03595; LFECT.
 DR ECGENE: EG11277; THRL.
 KW Threonine biosynthesis; Leader peptide.
 SO SEQUENCE 21 AA; 2138 MW; 6A9C9167F89ECC4 CRC64;

Query Match 40.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 37.5%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VSPVAPT 8
 : 1 1 :
 Db 4 ISTITTT 11

RESULT 12
 ID IBP2_PIG STANDARD; PRT; 23 AA.
 AC P24853;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 (IGFBP-2) (IBP-2)
 GN (IGF-BINDING PROTEIN 2) (FRAGMENT).
 OS IGFBP2.
 OC Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN (1)
 RP SEQUENCE.
 RX MEDLINE-92109718; PubMed-1722398;
 RA Coleman M.E., Pan Y.-C.E., Eberhart T.D.;
 RT "Identification and NH2-terminal amino acid sequence of three
 insulin-like growth factor-binding proteins in porcine serum.";
 RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
 AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
 CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
 CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- MISCELLANEOUS: BINDS IGF-II MORE THAN IGF-I.

CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY.
 DR PIR: JH0515; JH0515.
 DR INTERPRO: IPR00716; -
 DR INTERPRO: IPR000867; -
 DR PROSITE: PS00222; IGF_BINDING; PARTIAL.
 DR PROSITE: PS00484; THYROGLOBULIN_1; PARTIAL.
 KW Growth factor binding.
 FT NON_TER 23
 SO SEQUENCE 23 AA; 2387 MW; 731104B88825D2C4 CRC64;

Query Match 40.0%; Score 18; DB 1; Length 23;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 PVAP 7
 : 1 1 :
 Db 18 PAAP 21

RESULT 13
 ID MDH_PLAVE STANDARD; PRT; 24 AA.
 AC P19981;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN MDH.
 OS Plasmomonospora venezuelensis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptosporangineae; Streptosporangiaceae;
 OC Planomonospora.
 RN (1)
 RP SEQUENCE.
 RX MEDLINE-89374824; PubMed-2775496;
 RA Rommel T.O., Hund H.-K., Specht A.R., Lingens F.;
 RT "Purification and N-terminal amino-acid sequences of bacterial malate
 RT dehydrogenases from six actinomycetales strains and from
 RT phenylobacterium immobile, strain E.";
 RL Biol. Chem. Hoppe-Seyler 370:763-768(1989).
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR PIR: S04857; S04957.
 DR HSP: P10584; IBM.
 DR INTERPRO: IPR001236; -
 DR INTERPRO: IPR001252; -
 DR PFAM: PF00056; 1dh; 1.
 DR PROSITE: PS00068; MDH; PARTIAL.
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 24
 SO SEQUENCE 24 AA; 2475 MW; D8350129B9587C19 CRC64;

Query Match 40.0%; Score 18; DB 1; Length 24;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TPVAPT 8
 : 1 1 1 :
 Db 3 TPVAVT 8

RESULT 14
 ID MDH_STRRS STANDARD; PRT; 24 AA.
 AC P19983;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).

GN MDH.
OS Streptoporangium roseum.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptoporangineae; Streptoporangaceae;
OC Streptoporangium.
RN [1]
RP SEQUENCE
RX MEDLINE-89374824; PubMed-2775496;
RA Rommel T.O., Hund H.-K., Speith A.R., Jüngens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
dehydrogenases from six actinomycetales strains and from
RT phenyllobacterium immobile, strain F."
RL Biol. Chem. Hoppe-Seyler 370:763-768(1989).
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR PIR: S04956; S04956.
DR HSSP: P10584; IBDM.
DR INTERPRO: IPR001236; -.
DR INTERPRO: IPR001252; -.
DR PFAM: PF00056; Ldh; 1.
DR PROSITE: PS00068; MDH; PARTIAL.
KM Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 24 24
SQ SEQUENCE 24 AA: 2475 MM; D83501298587C19 CRC64;

Query Match 40.0%; Score 18; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TPVAPT 8
DB 3 TPVAVT 8

RESULT 15
TM2A_METMA STANDARD; PRT; 12 AA.
ID TM2A_METMA
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ALTERNATIVE TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 28 KDA SUBUNIT
DE (EC 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN-COENZYME M
DE METHYLTRANSFERASE 28 KDA SUBUNIT) (FRAGMENT).
OS Methanosarcina mazei.
OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
OC Methanosarcina.
RN [1]
RP SEQUENCE.
RC STRAIN-DSM 3647 / GOEL;
RX MEDLINE-96370840; PubMed-8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin;
RT coenzyme M methyltransferase from Methanosarcina mazei G01
RT reconstituted in ether lipid liposomes.";
RL Eur. J. Biochem. 239:857-864(1996).
CC -1- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -1- CATALYTIC ACTIVITY: 5-METHYL-5,6,7,8-TETRAHYDROMETHANOPTERIN +
CC 2-MERCAPTOETHANESULFONATE -> 5,6,7,8-TETRAHYDROMETHANOPTERIN +
CC 2-(METHYLTHIO)ETHANESULFONATE.
CC -1- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
KM Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT NON_TER 12 12
SQ SEQUENCE 12 AA: 1321 MM; 6DE4A5766232D76B CRC64;

Query Match 37.8%; Score 17; DB 1; Length 12;

Best Local Similarity 75.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 PVAP 7
DB 6 PVLP 9

Search completed: February 13, 2001, 13:06:53
Job time: 285 sec

THIS PAGE BLANK (USPTO)

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:01:18 ; Search time 58.16 Seconds

(without alignments)
18.137 Million cell updates/sec

Title: US-09-372-036-26

Perfect score: 43

Sequence: 1 VSTPVAPRQ 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 10868

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55.6	23	11	035829	035829 ratius norv
2	55.6	23	11	063334	063334 ratius norv
3	53.3	11	11	061797	061797 mus musculi
4	53.3	20	10	095870	095870 phleum prat
5	53.3	27	12	09YR04	09YR04 porcine cit
6	53.3	27	12	09YR06	09YR06 porcine cit
7	53.3	29	12	091863	091863 porcine cit
8	53.3	29	12	091866	091866 porcine cit
9	53.3	29	12	091869	091869 porcine cit
10	53.3	29	12	09YX00	09YX00 porcine cit
11	53.3	30	12	056130	056130 porcine cit
12	53.3	30	12	09YR10	09YR10 porcine cit
13	51.1	14	4	09UC70	09UC70 homo sapien
14	51.1	19	12	093210	093210 porcine cit
15	51.1	30	2	005845	005845 bordetella
16	48.9	23	11	P70635	P70635 ratius norv
17	48.9	24	2	09R516	09R516 pseudomonas
18	48.9	27	2	09R5D8	09R5D8 porphyromon
19	48.9	30	4	Q14579	Q14579 homo sapien

20	21.5	47.8	28	12	09WN13	09WN13 tt virus. o
21	21	46.7	16	2	09R4V4	09R4V4 pseudomonas
22	21	46.7	20	12	085636	085636 moloney mur
23	21	46.7	21	11	061917	061917 mus musculi
24	21	46.7	25	2	09KXX3	09KXX3 streptomyce
25	21	46.7	27	2	008674	008674 escherichia
26	21	46.7	27	10	039702	039702 datura immo
27	21	46.7	27	11	09QXD3	09QXD3 ratius norv
28	21	46.7	27	12	09J524	09J524 hepatitis c
29	21	46.7	27	12	09J523	09J523 hepatitis c
30	21	46.7	27	12	09J522	09J522 hepatitis c
31	21	46.7	27	12	09J520	09J520 hepatitis c
32	21	46.7	27	12	09J519	09J519 hepatitis c
33	21	46.7	27	12	09J5Y8	09J5Y8 hepatitis c
34	21	46.7	27	12	09J5Y7	09J5Y7 hepatitis c
35	21	46.7	27	12	09J156	09J156 hepatitis c
36	21	46.7	27	12	09J157	09J157 hepatitis c
37	21	46.7	28	2	09S1R3	09S1R3 streptomyce
38	21	46.7	29	8	063827	063827 melospiza g
39	21	46.7	29	8	063829	063829 melospiza g
40	21	46.7	29	8	063931	063931 melospiza g
41	21	46.7	29	12	086257	086257 human rotav
42	21	46.7	29	12	086259	086259 human rotav
43	21	46.7	29	12	086262	086262 human rotav
44	21	46.7	29	12	086256	086256 human rotav
45	21	46.7	29	12	086260	086260 human rotav

ALIGNMENTS

RESULT 1

035829 PRELIMINARY: PRT: 23 AA.

AC 035829; 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JAN-1998 (TREMBlrel. 05, Last annotation update)

DE LAMIN A (FRAGMENT).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;

RA Tivari B., Parnaik V.K.; to the EMBL/GenBank/DBJ databases.

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; Y15465; CAA75647.1; -

FT NON_TER

FT 23

SO SEQUENCE 23 AA; 2435 MW; 4E27DDA77E1925FE CRC64;

Query Match 55.6%; Score 25; DB 11; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 STVPAP 7
18 STPMSP 23

RESULT 2

063334 PRELIMINARY: PRT: 23 AA.

AC 063334; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE ALPHA-2-MACROGLOBULIN (FRAGMENT).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MISTAR;
 RX MEDLINE-85207604; PubMed-2581948;
 RA Northmann W., Helwig M., Kunz D., Heinrich P.C.;
 RT "Molecular cloning of cDNA sequences for rat alpha 2-macroglobulin and
 measurement of its transcription during experimental inflammation.";
 RL J. Biol. Chem. 260:6200-6205(1985).
 DR EMBL: M84369; AAA41594.1; -
 DR INTERPRO: IPR001599; -
 DR PFM: PFM00207; AZM: 1.
 FT NON_TER 1
 FT 23
 SQ SEQUENCE 23 AA; 2526 MW; E2D721FB1B23876 CRC64;

Query Match 55.6%; Score 25; DB 11; Length 23;
 Best Local Similarity 55.6%; Pred. No. 2.6e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 STRPVAP 9
 DB 14 LTRPAP 22

RESULT 3
 ID 061797 PRELIMINARY; PRT; 11 AA.
 AC 061797;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DE 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 RT HYPOTHEICAL PROTEIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1;
 RX MEDLINE-86215264; PubMed-3754749;
 RA Tanaka S., Fujimoto H.;
 RT "A postnecrotically expressed clone encodes lactate dehydrogenase
 RT isozyme X.";
 RL Biochem. Biophys. Res. Commun. 136:760-766(1986).
 DR EMBL: M12781; AAA8313.1; -
 KM Hypothetical protein.
 FT NON_TER 1
 FT 1
 SQ SEQUENCE 11 AA; 1122 MW; 32810C52476EA2D7 CRC64;

Query Match 53.3%; Score 24; DB 11; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 STRPVAP 7
 DB 1 MCTPVP 7

RESULT 4
 ID 0958Y0 PRELIMINARY; PRT; 20 AA.
 AC 0958Y0;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE ALLERGEN PHLP V (FRAGMENT).
 OS Phleum pratense (Common timothy).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Phleum.
 OX NCBI_TaxID-15957;

RN [1]
 RP SEQUENCE.
 RX MEDLINE-92353723; PubMed-1643437;
 RA Petersen A., Becker W.M., Schlaak M.;
 RT "Characterization of isoforms of the major allergen Phl p V by two-
 dimensional immunoblotting and microsequencing";
 RL Int. Arch. Allergy Immunol. 98:105-109(1992).
 SQ SEQUENCE 20 AA; 1832 MW; 05C17A6DCB4D9A12 CRC64;

Query Match 53.3%; Score 24; DB 10; Length 20;
 Best Local Similarity 66.7%; Pred. No. 3.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STRPVAP 7
 DB 8 ATPAP 13

RESULT 5
 ID 09YR04 PRELIMINARY; PRT; 27 AA.
 AC 09YR04;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE ORF-6.
 OS porcine circovirus type 2-E.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID-85344;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hamel A.L., Nayar G.P.S.;
 RT "Nucleotide sequence of four different isolates of circovirus detected
 in pigs with various clinical syndromes.";
 RT Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF109399; AAD03076.1; -
 SQ SEQUENCE 27 AA; 2748 MW; EED90E5C19D7CBDB CRC64;

Query Match 53.3%; Score 24; DB 12; Length 27;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STRPVAP 7
 DB 4 STRPAP 9

RESULT 6
 ID 09YOS6 PRELIMINARY; PRT; 27 AA.
 AC 09YOS6;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE ORF-6.
 OS porcine circovirus type 2-D.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID-86385;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hamel A.L., Nayar G.P.S.;
 RT "Genetic characterization of four novel type-2 porcine circoviruses.";
 RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF117753; AAD12316.1; -
 SQ SEQUENCE 27 AA; 2806 MW; EED90E5C19D10BDB CRC64;

Query Match 53.3%; Score 24; DB 12; Length 27;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
||| :1
Db 4 STPASP 9

RESULT 7

091863 ID 091863 PRELIMINARY; PRT; 29 AA.
AC 091863;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ORF6.
OS porcine circovirus.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
OX NCBI_TaxID=46221;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
RX MEDLINE=98418498; PubMed=9747726;
RA Meenan B.M., McNeilly F.M., Todd D., Kennedy S., Jewhurst V.,
RA Ellis J.A., Hassard L.E., Clark E.G., Haines D.M., Allan G.M.;
RT "Characterization of novel circovirus DNAs associated with wasting
RT syndromes in pigs.";
RL J. Gen. Virol. 79:2171-2199(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
RA Meenan B.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF055392; AAC35319.1; -
SO SEQUENCE 29 AA; 3009 MW; CA43AEC5FD1919CC CRC64;

Query Match

Best Local Similarity 53.3%; Score 24; DB 12; Length 29;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
||| :1
Db 4 STPASP 9

RESULT 8

091866 ID 091866 PRELIMINARY; PRT; 29 AA.
AC 091866;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ORF6.
OS porcine circovirus.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
OX NCBI_TaxID=46221;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
RX MEDLINE=98418498; PubMed=9747726;
RA Meenan B.M., McNeilly F.M., Todd D., Kennedy S., Jewhurst V.,
RA Ellis J.A., Hassard L.E., Clark E.G., Haines D.M., Allan G.M.;
RT "Characterization of novel circovirus DNAs associated with wasting
RT syndromes in pigs.";
RL J. Gen. Virol. 79:2171-2199(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
RA Meenan B.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF055393; AAC35329.1; -
SO SEQUENCE 29 AA; 3040 MW; 7E43AED2621919D1 CRC64;

Query Match

53.3%; Score 24; DB 12; Length 29;

Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
||| :1
Db 4 STPASP 9

RESULT 9

091869 ID 091869 PRELIMINARY; PRT; 29 AA.
AC 091869;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ORF6.
OS porcine circovirus.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
OX NCBI_TaxID=46221;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
RX MEDLINE=98418498; PubMed=9747726;
RA Meenan B.M., McNeilly F.M., Todd D., Kennedy S., Jewhurst V.,
RA Ellis J.A., Hassard L.E., Clark E.G., Haines D.M., Allan G.M.;
RT "Characterization of novel circovirus DNAs associated with wasting
RT syndromes in pigs.";
RL J. Gen. Virol. 79:2171-2199(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
RA Meenan B.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF055394; AAC35339.1; -
SO SEQUENCE 29 AA; 3039 MW; 4843AED2621919D9 CRC64;

Query Match

Best Local Similarity 53.3%; Score 24; DB 12; Length 29;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
||| :1
Db 4 STPASP 9

RESULT 10

09Y0X0 ID 09Y0X0 PRELIMINARY; PRT; 29 AA.
AC 09Y0X0;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE ORF-6.
OS porcine circovirus type 2-B.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
OX NCBI_TaxID=85709;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamel A.L., Nayar G.P.S.;
RT "Nucleotide sequence of four different isolates of porcine circovirus
RT detected in pigs with various clinical syndromes.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF112862; AAD03084.1; -
SO SEQUENCE 29 AA; 3092 MW; CA43AED90ESC19CC CRC64;

Query Match

Best Local Similarity 53.3%; Score 24; DB 12; Length 29;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
||| :1

Db 4 STPASP 9

RESULT 11

AC 056130 PRELIMINARY; PRT; 29 AA.
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE STRAIN PMWS PCV, COMPLETE GENOME (ORF-6).
 OS Porcine circovirus, and bovine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=46221, 85542;
 RN [1]
 RP SPECIES-Porcine circovirus; STRAIN-PMWS PCV;
 RC MEDLINE=98241772; PubMed=9573301;
 RA Hamel A.L., Lin L.L., Nayar G.P.S.;
 RT "Nucleotide sequence of porcine circovirus associated with postweaning
 RT multisystemic wasting syndrome in pigs.";
 RL J. Virol. 72:5262-5267(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Porcine circovirus; STRAIN-PMWS PCV;
 RA Hamel A.L., Lin L.L., Nayar G.P.S.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Porcine circovirus; STRAIN-PORCINE CIRCOVIRUS TYPE II;
 RA MEDLINE=98418498; PubMed=9747726;
 RA Meenan B.M., McNeilly F.M., Todd D., Kennedy S., Jewhurst V.,
 RA Ellis J.A., Hassard L.E., Clark E.G., Haines D.M., Allan G.M.;
 RT "Characterization of novel circovirus DNAs associated with wasting
 RT syndromes in pigs.";
 RL J. Gen. Virol. 79:2171-2199(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Porcine circovirus; STRAIN-PORCINE CIRCOVIRUS TYPE II;
 RA Meenan B.M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine circovirus;
 RA Hamel A.L., Nayar G.P.S.;
 RT "Nucleotide sequence of a circovirus detected in cattle with various
 RT clinical syndromes.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF027217; AAC59467.1; -;
 DR EMBL; AF055391; AAC35308.1; -;
 DR EMBL; AF109397; AAD11933.1; -;
 SQ SEQUENCE 29 AA; 3093 MW; 7E43AED905C19D1 CRC64;

Query Match 53.3%; Score 24; DB 12; Length 29;
 Best Local Similarity 66.7%; Pred. No. 5e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPASP 7
 III:1
 Db 4 STPASP 9

RESULT 12

OYR10 PRELIMINARY; PRT; 30 AA.
 AC 09YR10;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE ORF-6.
 OS Porcine circovirus type 2-C.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.

OX NCBI_TaxID=85543;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Hamel A.L., Nayar G.P.S.;
 RT "Nucleotide sequence of four different isolates of circovirus detected
 RT in pigs with various clinical syndromes.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF109398; AAD03066.1; -;
 SQ SEQUENCE 30 AA; 3197 MW; C01E43AED905C19 CRC64;

Query Match 53.3%; Score 24; DB 12; Length 30;
 Best Local Similarity 66.7%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPASP 7
 III:1
 Db 4 STPASP 9

RESULT 13

OYR10 PRELIMINARY; PRT; 14 AA.
 AC 09UCTO;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE BASIC PROLINE-RICH PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92082469; PubMed=1747107;
 RA Ramasubbu N., Reddy M.S., Bergey E.J., Haraszthy G.G., Sonl S.D.,
 RA Levine M.J.;
 RT "Large-scale purification and characterization of the major
 RT phosphoproteins and mucins of human submandibular-sublingual saliva.";
 RL Biochem. J. 280:341-352(1991).
 RL Biochem. J. 280:341-352(1991).
 SQ SEQUENCE 14 AA; 1435 MW; DC513E0923990A6D CRC64;

Query Match 51.1%; Score 23; DB 4; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PVAPQ 9
 III:1
 Db 5 PLAPQ 10

RESULT 14

OYR10 PRELIMINARY; PRT; 19 AA.
 AC 093210;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE ORF7.
 OS Porcine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=46221;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
 RX MEDLINE=98418498; PubMed=9747726;
 RA Meenan B.M., McNeilly F.M., Todd D., Kennedy S., Jewhurst V.,
 RA Ellis J.A., Hassard L.E., Clark E.G., Haines D.M., Allan G.M.;
 RT "Characterization of novel circovirus DNAs associated with wasting
 RT syndromes in pigs.";
 RL J. Gen. Virol. 79:2171-2199(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
 RA Meenan B.M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF055394; AAC35338.1; -
 DR EMBL: AF055393; AAC35328.1; -
 SQ SEQUENCE 19 AA; 1977 MW; 2DBAAB58EFAA923 CRC64;

Query Match 51.1%; Score 23; DB 12; Length 19;
 Best Local Similarity 66.7%; Pred. No. 5.1e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 STPVAP 7
 11111

Db 8 SSPVTP 13

RESULT 15

ID Q05845 PRELIMINARY; PRT; 30 AA.
 AC Q05845;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE VRG73 PROTEIN (FRAGMENT).
 GN VRG73.
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 OC Bordetella.
 OX NCBI_TaxID=520;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93123171; Pubmed=8419298;
 RA Beattie D.T., Mahan M.J., Mekalanos J.J.;
 RT "Repressor binding to a regulatory site in the DNA coding sequence is
 sufficient to confer transcriptional regulation of the vir-repressed
 RT genes (vrG genes) in Bordetella pertussis.";
 RL J. Bacteriol. 175:519-527(1993).
 CC -1- MISCELLANEOUS: THIS IS A VIR-REPPRESSED GENE (VRG) PROTEIN WHOSE
 CC EXPRESSION IS INDIRECTLY REPPRESSED BY THE BORDETELLA VIRULENCE
 CC GENE VIR (BVG).
 CC EMBL: L06123; AAA22989.1; -
 DR NON_TER 30
 FT 30
 SO SEQUENCE 30 AA; 3245 MW; 216787B0D78CE28 CRC64;

Query Match 51.1%; Score 23; DB 2; Length 30;
 Best Local Similarity 66.7%; Pred. No. 8e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VSTPVA 6
 11111

Db 9 VQTPVA 14

Search completed: February 13, 2001, 13:06:28
 Job time: 310 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:03:16 ; Search time 32.52 Seconds
(without alignments)
6.074 Million cell updates/sec

Title: US-09-372-036-29
Perfect score: 57
Sequence: 1 000TAPKAPTE 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 111283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCMus_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57	100.0	11	2	US-08-456-670B-29	Sequence 29, Appl
2	57	100.0	12	2	US-08-456-670B-42	Sequence 42, Appl
3	57	100.0	21	1	US-08-127-499A-33	Sequence 33, Appl
4	57	100.0	21	1	US-08-482-847-33	Sequence 33, Appl
5	47	82.5	23	2	US-08-456-670B-20	Sequence 20, Appl
6	39	68.4	11	2	US-08-456-670B-38	Sequence 38, Appl
7	35	61.4	7	1	US-08-127-499A-34	Sequence 34, Appl
8	35	61.4	7	1	US-08-482-847-34	Sequence 34, Appl
9	35	61.4	9	2	US-08-456-670B-25	Sequence 25, Appl
10	33	57.9	15	2	US-08-934-915-72	Sequence 72, Appl
11	28	49.1	21	2	US-08-560-558E-2	Sequence 2, Appl
12	28	49.1	24	2	US-08-726-306A-171	Sequence 171, App
13	27	47.4	22	2	US-08-481-793-36	Sequence 36, Appl
14	27	47.4	22	2	US-08-354-326-36	Sequence 36, Appl
15	27	47.4	22	4	PCT-US95-07068-36	Sequence 36, Appl
16	27	47.4	22	4	US-08-459-568-44	Sequence 44, Appl
17	27	47.4	29	2	US-08-459-568-45	Sequence 45, Appl
18	27	47.4	29	2	US-08-399-411-44	Sequence 44, Appl
19	27	47.4	29	2	US-08-399-411-45	Sequence 45, Appl
20	27	47.4	29	3	US-08-516-859A-44	Sequence 44, Appl
21	27	47.4	29	3	US-08-516-859A-45	Sequence 45, Appl
22	26	45.6	9	4	US-08-340-283-34	Sequence 34, Appl
23	26	45.6	9	4	PCT-US95-16415-19	Sequence 19, Appl
24	26	45.6	13	2	US-08-456-670B-36	Sequence 36, Appl
25	26	45.6	24	3	US-09-136-251-5	Sequence 5, Appl
26	26	45.6	25	2	US-08-396-452-5	Sequence 5, Appl
27	26	45.6	25	2	US-08-456-670B-23	Sequence 23, Appl
28	25	43.9	11	3	US-09-142-759-7	Sequence 7, Appl

29	25	43.9	13	1	US-08-477-509B-20	Sequence 20, Appl
30	25	43.9	15	3	US-08-167-867-11	Sequence 11, Appl
31	25	43.9	16	1	US-08-463-862-7	Sequence 7, Appl
32	25	43.9	16	2	US-08-458-887-7	Sequence 7, Appl
33	25	43.9	17	1	US-07-915-919-1	Sequence 1, Appl
34	25	43.9	17	1	US-08-205-938A-36	Sequence 36, Appl
35	25	43.9	17	1	US-08-205-938A-38	Sequence 38, Appl
36	25	43.9	17	1	US-08-271-162-1	Sequence 1, Appl
37	25	43.9	17	1	US-08-271-162-2	Sequence 2, Appl
38	25	43.9	17	1	US-08-271-162-3	Sequence 3, Appl
39	25	43.9	17	1	US-08-271-162-4	Sequence 4, Appl
40	25	43.9	17	4	PCT-US95-02626-36	Sequence 36, Appl
41	25	43.9	17	4	PCT-US95-02626-38	Sequence 38, Appl
42	25	43.9	17	4	PCT-US95-08302-1	Sequence 1, Appl
43	25	43.9	17	4	PCT-US95-08302-2	Sequence 2, Appl
44	25	43.9	17	4	PCT-US95-08302-3	Sequence 3, Appl
45	25	43.9	17	4	PCT-US95-08302-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-456-670B-29
Sequence 29, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
SPRAIN: EGD
US-08-456-670B-29

Query Match 100.0%; Score 57; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
|||||
DB 1 QOOTAPKAPTE 11

RESULT 2
US-08-456-670B-42
Sequence 42, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HANLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-456-670B-42

Query Match 100.0%; Score 57; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
|||||
DB 2 QOOTAPKAPTE 12

RESULT 3
US-08-127-499A-33
Sequence 33, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-33

Query Match 100.0%; Score 57; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
|||||
DB 7 QOOTAPKAPTE 17

RESULT 4

US-08-482-847-33
; Sequence 33, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE//DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-482-847-33

Query Match 100.0%; Score 57; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OOOTAPKAPTE 11
Db 7 OOOTAPKAPTE 17

RESULT 5
; Sequence 20, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAMELZIK, MARTINA
; APPLICANT: LINNWEILER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,670B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/412,227
; FILING DATE: 27-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE//DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1-7
; OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
; OTHER INFORMATION: MAY BE ABSENT"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 17-23
; OTHER INFORMATION: /note= "SOME OR ALL Xaa AMINO ACIDS
; OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-20

Query Match 82.5%; Score 47; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OOOTAPKAPT 10
Db 8 OOOTAPKAPT 16

RESULT 6
; Sequence 38, Application US/08456670B
; Patent No. 5932415
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED

APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: COBBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAWLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ. ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria innocua
US-08-456-670B-38

Query Match 68.4%; Score 39; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.48;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOOTAPKAPTE 11
DB 1 EQOTTKAPTO 11

RESULT 7
US-08-127-499A-34
Sequence 34, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra

TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-34

Query Match 61.4%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOOTAPKA 8
DB 1 QOOTAPKA 7

RESULT 8
US-08-482-847-34
Sequence 34, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499

FILED DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-34

Query Match 61.4%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOTAPKA 8
1111111
Db 1 QOTAPKA 7

RESULT 9

US-08-456-670B-25
Sequence 25, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFFRIED
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-25

Query Match 61.4%; Score 35; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QOTAPKAPT 10
1111111
Db 1 QOTTTKAPT 9

RESULT 10

US-08-934-915-72
Sequence 72, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILNER, JOAKIM
APPLICANT: DILNER, LENA
APPLICANT: CHENG, HWE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNASSAY FOR
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946,6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354,326
FILING DATE: 12-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: IGI-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-481-793-36

Query Match 47.4%; Score 27; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TAPKAP 9
|||||
DB 2 TAPKIP 7

RESULT 14
US-08-354-326-36
Sequence 36, Application US/08354326
Patent No. 5912121
GENERAL INFORMATION:
APPLICANT: SEIDMAN, C.E. ET AL.
TITLE OF INVENTION: METHODS FOR DETECTING MUTATIONS ASSOCIATED WITH
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/354,326
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: IGI-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-354-326-36

Query Match 47.4%; Score 27; DB 2; Length 22;

Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TAPKAP 9
|||||
DB 2 TAPKIP 7

RESULT 15
PCT-US95-07068-36
Sequence 36, Application PC/TUS9507068
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR DETECTING MUTATIONS ASSOCIATED WITH
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07068
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,326
FILING DATE: 12-DEC-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,627
FILING DATE: 02-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: IGI-037CNPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT-US95-07068-36

Query Match 47.4%; Score 27; DB 4; Length 22;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TAPKAP 9
|||||
DB 2 TAPKIP 7

Search completed: February 13, 2001, 13:03:17
Job time: 157 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:02:01 ; Search time 44.34 Seconds
(without alignments)
8.483 Million cell updates/sec

Title: US-09-372-036-29
Perfect score: 57
Sequence: 1 000TAPKAPTE 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 151408

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	11	14	AA1980.DAT
2	57	100.0	21	16	AA1981.DAT
3	47	82.5	9	14	AA1982.DAT
4	47	82.5	23	14	AA1983.DAT
5	39	68.4	11	14	AA1984.DAT
6	35	61.4	7	16	AA1985.DAT
7	35	61.4	9	14	AA1986.DAT
8	35	61.4	23	14	AA1987.DAT
9	33	57.9	21	12	AA1988.DAT
10	30	52.6	30	20	AA1989.DAT
11	29	50.9	14	21	AA1990.DAT
12	28	49.1	14	21	AA1991.DAT

Result No.	Score	Query Match	Length	ID	Description
13	28	49.1	15	17	AA1992.DAT
14	28	49.1	13	16	AA1993.DAT
15	27	47.4	14	16	AA1994.DAT
16	27	47.4	14	21	AA1995.DAT
17	27	47.4	14	21	AA1996.DAT
18	27	47.4	15	20	AA1997.DAT
19	27	47.4	15	21	AA1998.DAT
20	27	47.4	19	19	AA1999.DAT
21	27	47.4	19	19	AA2000.DAT
22	27	47.4	20	21	AA2001.DAT
23	27	47.4	26	16	AA2002.DAT
24	26	45.6	9	15	AA2003.DAT
25	26	45.6	9	17	AA2004.DAT
26	26	45.6	17	17	AA2005.DAT
27	26	45.6	11	14	AA2006.DAT
28	26	45.6	12	14	AA2007.DAT
29	26	45.6	12	14	AA2008.DAT
30	26	45.6	12	18	AA2009.DAT
31	26	45.6	12	18	AA2010.DAT
32	26	45.6	12	18	AA2011.DAT
33	26	45.6	12	21	AA2012.DAT
34	26	45.6	12	21	AA2013.DAT
35	26	45.6	13	14	AA2014.DAT
36	26	45.6	14	18	AA2015.DAT
37	26	45.6	14	21	AA2016.DAT
38	26	45.6	14	21	AA2017.DAT
39	26	45.6	15	18	AA2018.DAT
40	26	45.6	15	21	AA2019.DAT
41	26	45.6	17	19	AA2020.DAT
42	26	45.6	17	19	AA2021.DAT
43	26	45.6	20	17	AA2022.DAT
44	26	45.6	20	19	AA2023.DAT
45	26	45.6	24	20	AA2024.DAT

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	11	14	AA1980.DAT
2	57	100.0	21	16	AA1981.DAT
3	47	82.5	9	14	AA1982.DAT
4	47	82.5	23	14	AA1983.DAT
5	39	68.4	11	14	AA1984.DAT
6	35	61.4	7	16	AA1985.DAT
7	35	61.4	9	14	AA1986.DAT
8	35	61.4	23	14	AA1987.DAT
9	33	57.9	21	12	AA1988.DAT
10	30	52.6	30	20	AA1989.DAT
11	29	50.9	14	21	AA1990.DAT
12	28	49.1	14	21	AA1991.DAT
13	28	49.1	15	17	AA1992.DAT
14	28	49.1	13	16	AA1993.DAT
15	27	47.4	14	16	AA1994.DAT
16	27	47.4	14	21	AA1995.DAT
17	27	47.4	14	21	AA1996.DAT
18	27	47.4	15	20	AA1997.DAT
19	27	47.4	15	21	AA1998.DAT
20	27	47.4	19	19	AA1999.DAT
21	27	47.4	19	19	AA2000.DAT
22	27	47.4	20	21	AA2001.DAT
23	27	47.4	26	16	AA2002.DAT
24	26	45.6	9	15	AA2003.DAT
25	26	45.6	9	17	AA2004.DAT
26	26	45.6	17	17	AA2005.DAT
27	26	45.6	11	14	AA2006.DAT
28	26	45.6	12	14	AA2007.DAT
29	26	45.6	12	14	AA2008.DAT
30	26	45.6	12	18	AA2009.DAT
31	26	45.6	12	18	AA2010.DAT
32	26	45.6	12	18	AA2011.DAT
33	26	45.6	12	21	AA2012.DAT
34	26	45.6	12	21	AA2013.DAT
35	26	45.6	13	14	AA2014.DAT
36	26	45.6	14	18	AA2015.DAT
37	26	45.6	14	21	AA2016.DAT
38	26	45.6	14	21	AA2017.DAT
39	26	45.6	15	18	AA2018.DAT
40	26	45.6	15	21	AA2019.DAT
41	26	45.6	17	19	AA2020.DAT
42	26	45.6	17	19	AA2021.DAT
43	26	45.6	20	17	AA2022.DAT
44	26	45.6	20	19	AA2023.DAT
45	26	45.6	24	20	AA2024.DAT

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	11	14	AA1980.DAT
2	57	100.0	21	16	AA1981.DAT
3	47	82.5	9	14	AA1982.DAT
4	47	82.5	23	14	AA1983.DAT
5	39	68.4	11	14	AA1984.DAT
6	35	61.4	7	16	AA1985.DAT
7	35	61.4	9	14	AA1986.DAT
8	35	61.4	23	14	AA1987.DAT
9	33	57.9	21	12	AA1988.DAT
10	30	52.6	30	20	AA1989.DAT
11	29	50.9	14	21	AA1990.DAT
12	28	49.1	14	21	AA1991.DAT
13	28	49.1	15	17	AA1992.DAT
14	28	49.1	13	16	AA1993.DAT
15	27	47.4	14	16	AA1994.DAT
16	27	47.4	14	21	AA1995.DAT
17	27	47.4	14	21	AA1996.DAT
18	27	47.4	15	20	AA1997.DAT
19	27	47.4	15	21	AA1998.DAT
20	27	47.4	19	19	AA1999.DAT
21	27	47.4	19	19	AA2000.DAT
22	27	47.4	20	21	AA2001.DAT
23	27	47.4	26	16	AA2002.DAT
24	26	45.6	9	15	AA2003.DAT
25	26	45.6	9	17	AA2004.DAT
26	26	45.6	17	17	AA2005.DAT
27	26	45.6	11	14	AA2006.DAT
28	26	45.6	12	14	AA2007.DAT
29	26	45.6	12	14	AA2008.DAT
30	26	45.6	12	18	AA2009.DAT
31	26	45.6	12	18	AA2010.DAT
32	26	45.6	12	18	AA2011.DAT
33	26	45.6	12	21	AA2012.DAT
34	26	45.6	12	21	AA2013.DAT
35	26	45.6	13	14	AA2014.DAT
36	26	45.6	14	18	AA2015.DAT
37	26	45.6	14	21	AA2016.DAT
38	26	45.6	14	21	AA2017.DAT
39	26	45.6	15	18	AA2018.DAT
40	26	45.6	15	21	AA2019.DAT
41	26	45.6	17	19	AA2020.DAT
42	26	45.6	17	19	AA2021.DAT
43	26	45.6	20	17	AA2022.DAT
44	26	45.6	20	19	AA2023.DAT
45	26	45.6	24	20	AA2024.DAT

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	11	14	AA1980.DAT
2	57	100.0	21	16	AA1981.DAT
3	47	82.5	9	14	AA1982.DAT
4	47	82.5	23	14	AA1983.DAT
5	39	68.4	11	14	AA1984.DAT
6	35	61.4	7	16	AA1985.DAT
7	35	61.4	9	14	AA1986.DAT
8	35	61.4	23	14	AA1987.DAT
9	33	57.9	21	12	AA1988.DAT
10	30	52.6	30	20	AA1989.DAT
11	29	50.9	14	21	AA1990.DAT
12	28	49.1	14	21	AA1991.DAT
13	28	49.1	15	17	AA1992.DAT
14	28	49.1	13	16	AA1993.DAT
15	27	47.4	14	16	AA1994.DAT
16	27	47.4	14	21	AA1995.DAT
17	27	47.4	14	21	AA1996.DAT
18	27	47.4	15	20	AA1997.DAT
19	27	47.4	15	21	AA1998.DAT
20	27	47.4	19	19	AA1999.DAT
21	27	47.4	19	19	AA2000.DAT
22	27	47.4	20	21	AA2001.DAT
23	27	47.4	26	16	AA2002.DAT
24	26	45.6	9	15	AA2003.DAT
25	26	45.6	9	17	AA2004.DAT
26	26	45.6	17	17	AA2005.DAT
27	26	45.6	11	14	AA2006.DAT
28	26	45.6	12	14	AA2007.DAT
29	26	45.6	12	14	AA2008.DAT
30	26	45.6	12	18	AA2009.DAT
31	26	45.6	12	18	AA2010.DAT
32	26	45.6	12	18	AA2011.DAT
33	26	45.6	12	21	AA2012.DAT
34	26	45.6	12	21	AA2013.DAT
35	26	45.6	13	14	AA2014.DAT
36	26	45.6	14	18	AA2015.DAT
37	26	45.6	14	21	AA2016.DAT
38	26	45.6	14	21	AA2017.DAT
39	26	45.6	15	18	AA2018.DAT
40	26	45.6	15	21	AA2019.DAT
41	26	45.6	17	19	AA2020.DAT
42	26	45.6	17	19	AA2021.DAT
43	26	45.6	20	17	AA2022.DAT
44	26	45.6	20	19	AA2023.DAT
45	26	45.6	24	20	AA2024.DAT

XX Key Location/Qualifiers
 FH Region 1..7
 FT /note= "opt. 0-7 amino acid residues"
 FT Region 17..23
 FT /note= "opt. 0-7 amino acid residues"
 XX
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERCK) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Claim 3; Page 4; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 XX
 SQ Sequence 23 AA:
 Query Match 82.5%; Score 47; DB 14; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QQTAPKAPT 10
 |||||
 Db 8 qqtapkapt 16
 RESULT 5
 R54627
 ID R54627 standard; Protein; 11 AA.
 XX
 AC R54627;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria innocua p60 peptide epitope.
 XX
 KW Antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERCK) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;

PI Hoffmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure; Fig 5; 19pp; German.
 XX
 CC The sequence is that of a Listeria innocua p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species.
 XX
 SQ Sequence 11 AA:
 Query Match 68.4%; Score 39; DB 14; Length 11;
 Best Local Similarity 63.6%; Pred. No. 0.87;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQTAPKAPTE 11
 :||| ||||
 Db 1 eqtttkaptq 11
 RESULT 6
 R73906
 ID R73906 standard; peptide; 7 AA.
 XX
 AC R73906;
 XX
 DT 05-DEC-1995 (first entry)
 XX
 DE Listeria monocytogenes protein p60 precursor peptide 292-298.
 XX
 KW Listeria monocytogenes; protein p60 precursor; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KW viral; peptide 292-298.
 XX
 OS Listeria monocytogenes.
 XX
 PN W09509232-A.
 XX
 PD 06-APR-1995.
 XX
 PF 28-SEP-1994; 94WO-CA00516.
 XX
 PR 28-SEP-1993; 93US-0127499.
 XX
 PA (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 PI Sharma LR, Van Alstyne D;
 XX
 DR WPI; 1995-147431/19.
 XX
 PT New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 PS Claim 35; Page 77; 98pp; English.
 XX
 CC R73913 is the Listeria monocytogenes protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in R73891-R73894 and R73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,

CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 XX
 SQ Sequence 7 AA;

Query Match 61.4%; Score 35; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QOTAPKA 8
 DB 1 qqtapka 7

RESULT 7
 R54623
 ID R54623 standard: Protein; 9 AA.
 AC R54623;
 XX
 DT 16-JUN-1994 (first entry)
 DE Listeria p60 peptide epitope.
 XX
 KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 PN DE4318450-A.
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERCK) MERCK PATENT GMBH.
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure; Page 3; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 XX
 SQ Sequence 9 AA;

Query Match 61.4%; Score 35; DB 14; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2.1e+05;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 QOTAPKAPT 10
 DB 1 qqtckapt 9
 RESULT 8
 R45167
 ID R45167 standard: Protein; 23 AA.
 XX

AC R45167;
 XX
 DT 16-JUN-1994 (first entry)
 DE Listeria p60 peptide epitope.
 XX
 KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Region 1..7
 FT /note= "opt. 0-7 amino acid residues"
 FT 17..23
 FT Region /note= "opt. 0-7 amino acid residues"
 XX
 PN DE4318450-A.
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERCK) MERCK PATENT GMBH.
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Claim 3; Page 4; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 XX
 SQ Sequence 23 AA;

Query Match 61.4%; Score 35; DB 14; Length 23;
 Best Local Similarity 77.8%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 QOTAPKAPT 10
 DB 8 qqtckapt 16

RESULT 9
 R15594
 ID R15594 standard: Protein; 21 AA.
 AC R15594;
 XX
 DT 02-MAR-1992 (first entry)
 DE Immunopeptide derived from HPV31 L1 peptide.
 XX
 KW cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
 KW squamous cell carcinoma; ELISA; HPV 31.
 XX
 OS Synthetic.
 XX
 PN WO9118294-A.
 XX

PD 28-NOV-1991.
 XX
 PF 13-MAY-1991: 91WO-SE00335.
 XX
 PR 11-MAY-1990: 90SE-0001705.
 XX
 PA (MEDS-) MEDSCAND AB.
 XX
 PI Dillner J, Dillner L, Cheng HM;
 DR WPI: 1991-369390/50.
 XX
 PT Diagnosis of human papilloma virus infection and PV-carrying
 PT tumours - using synthetic peptide(s) to detect virus specific
 PT antigen-antibody complexes by immunoassay
 XX
 PS Disclosure: Page 39; 72pp: English.
 XX
 CC This is one of a large number of peptides which have been
 CC synthesised on the basis of the amino acid sequences for the E2, E4,
 CC E7, E1 or E2 proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The
 CC selection of peptide sequences was based on the assumption that an
 CC immunoreactive region might be situated in the same relative region
 CC of a protein from different HPV types. The peptides were used in
 CC diagnostic immunoassays to detect HPV-infection.
 CC See R15523-R15601.
 CC
 XX
 SO Sequence 21 AA:
 Query Match 57.9%; Score 33; DB 12; Length 21;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OY 2 QOTAPKAPTE-11
 Db 8 qktapqkpkke 17
 XX
 RESULT 10
 Y09351
 ID Y09351 standard; peptide: 30 AA.
 XX
 AC Y09351;
 XX
 DT 09-JUL-1999 (first entry)
 DE Rat RAGE V-domain peptide SEQ ID NO:3.
 XX
 KW RAGE; V-domain; receptor for advanced glycation endproduct;
 KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
 KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
 KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KW tumour; cancer; male impotence; wound healing; periodontal disease;
 KW neuropathy; retinopathy; nephropathy; neuronal degeneration.
 XX
 OS Rattus sp.
 XX
 PN W09918987-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998: 98WO-US21346.
 XX
 PR 09-OCT-1997: 97US-0948131.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Lamster I, Schmidt AM, Stern D, Yan SD;
 XX
 DR WPI: 1999-277439/23.
 XX

PT New peptides based on an advanced glycation end product receptor are
 PT useful for treating Alzheimer's disease and Down's syndrome
 XX
 PS Claim 4; Page 78; 101pp: English.
 XX
 CC The present invention describes novel isolated peptides (I) having an
 CC amino acid sequence corresponding to an amino acid sequence of a
 CC V-domain of a receptor for an advanced glycation end product (RAGE).
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a
 CC microglial cell by an ABP; (8) treating a subject with a condition
 CC associated with an interaction of an ABP with a receptor for RAGE on a
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
 CC with a receptor for RAGE when the receptor is on the surface of a cell;
 CC and (13) treating a subject with a condition associated with an
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
 CC can be used for treating conditions associated with an interaction of an
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
 CC or neuronal degeneration.
 CC
 XX
 SO Sequence 30 AA:
 Query Match 52.6%; Score 30; DB 20; Length 30;
 Best Local Similarity 55.6%; Pred. No. 76;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OY 3 QTPAKAPTE 11
 Db 17 kaapkkpqc 25
 XX
 RESULT 11
 Y99219
 ID Y99219 standard; Peptide: 14 AA.
 XX
 AC Y99219;
 XX
 DT 07-AUG-2000 (first entry)
 DE HLA class II binding antigen epitope peptide #408.
 XX
 KW Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
 KW immune response; chronic viral disease; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
 KW allograft rejection; allergy; Lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.
 XX
 OS Unidentified.
 XX
 PN W09961916-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999: 99WO-US12066.
 XX
 PR 29-MAY-1998: 98US-0087192.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX

P1	Sette A, Southwood S, Sidney J;
XX	
DR	WPI: 2000-097143/08.
PT	New compositions containing immunogenic peptide epitopes for various
XX	HLA class II DR molecules useful for inducing helper T cell response
PS	Claim 1; Page 46; 60pp; English.
XX	
CC	The present invention relates to a new pharmaceutical composition
CC	comprising a unit dose form of a peptide, or analogue, comprising an
CC	epitope selected from those represented by peptides Y98812-Y99339 which
CC	are derived from various antigens for various human leucocyte antigen
CC	class DR molecules, representative of the world wide population. The
CC	peptide/analogue binds to an HLA class II molecule at an IC-50 of less
CC	than or equal to 1,000 nM. The pharmaceutical can be used to induce a
CC	helper T cell response. The pharmaceutical focuses the immune response
CC	towards selected determinants and could therefore be used in cases of
CC	chronic viral diseases and cancer. Examples of diseases that can be
CC	treated using the peptide containing pharmaceutical include autoimmune
CC	diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
CC	gravis), allograft rejection, allergies, Lyme disease, hepatitis,
CC	post-streptococcal endocarditis or glomerulonephritis and food
CC	hypersensitivities. The peptide epitopes can be used to enhance immune
CC	responses against other immunogens administered with the peptides.
CC	Diseases which can be treated using immunogenic mixtures include prostate
CC	cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
CC	carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
CC	used to make monoclonal antibodies useful as potential diagnostic or
CC	therapeutic agents. The peptides may also be useful as diagnostic
CC	reagents, for example, to determine the susceptibility of an individual
CC	to a treatment regimen. Also, the peptides may be used to predict which
CC	individuals will be at substantial risk of developing chronic infection.
CC	The selection of appropriate T and B cell epitopes should allow the
CC	development of epitope based vaccines particularly towards conserved
CC	epitopes of pathogens which are characterized by high sequence
CC	variability such as HIV, HCV and Malaria.
SQ	Sequence 14 AA:
OY	1 QOOTAPKAPT 10 Db 5 qsgtalrkakt 14
RESULT 12	
ID y51019	y51019 standard; peptide; 14 AA.
CC y51019:	
DT 17-MAR-2000	(first entry)
DE EBVA derived control peptide fragment #1.	
KW Epitope; Kaposi sarcoma; anti-HHV8 antibody; detection; human.	
OS Epstein Barr virus.	
PN MO9962938-AZ.	
PD 09-DEC-1999.	
PF 28-MAY-1999;	99WO-EP03719.
PR 29-MAY-1998;	98DE-1024244.
PA (SCHA/) SCHATZ O.	

PA	(HAAS//)HAAS J.
PI	Schatz O, Haas J;
PR	WPI: 2000-072830/06.
DR	
XX	
XX	Polypeptides that are recognized by antibodies against human herpes
PT	virus-8, used for diagnosis, prevention and treatment of HHV8
PN	infections, e.g. Kaposi sarcoma -
XX	
PS	Example 4; Page 25; 39pp; German.
XX	
CC	This invention describes novel non-naturally occurring human herpes
CC	virus-8 (HHV8) polypeptides (I), that are recognized by anti-HHV8
CC	antibodies from infected patients. The peptides of the invention have
CC	antiviral, cytostatic and immunostimulatory activity. (I), polymers
CC	containing (I), their fusion proteins and conjugates, are used for
CC	treatment of the HHV8 associated diseases, especially Kaposi sarcoma,
CC	Castleman's disease, primary effusion lymphoma, interstitial pneumonia,
CC	encephalitis and multiple myeloma, for production of antibodies (e.g. as
CC	vaccines); and for the diagnostic detection of anti-HHV8 antibodies (e.g.
CC	including blood screening). (II) provide a more specific, sensitive and
CC	reproducible method for the detection of anti-HHV8 antibodies (Ab), than
CC	current methods (e.g. 96% of Kaposi sarcoma patients tested positive).
CC	Using several different (I) allows detection of a wide range of different
CC	Ab (particularly important in immune deficient patients), and since (I)
CC	are synthetic, the difficulties of purifying recombinant antigens, and
CC	possible contamination by host cell proteins, are avoided. Y51010-Y51020
CC	represent the peptides described in the method of the invention.
XX	
SO	Sequence 14 AA:
	Query Match 49.1%; Score 28; DB 21; Length 14;
	Best Local Similarity 55.6%; Pred. No. 77;
	Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0
OY	1 QOQTAPKAP 9
	: : : :
DB	5 gepapgap 13
RESULT 13	
R96287	
ID	R96287 standard; peptide; 15 AA.
AC	
XX	R96287;
XX	
DT	07-JAN-1997 (first entry)
DE	
XX	Light chain framework region 2 for human EGF-R antibody.
XX	
KW	Antibody: Ab; human; EGF-R; epidermal growth factor receptor; monoclonal;
KW	humanised antibody; framework region; antigen binding site; light chain;
KW	CDR; heavy chain; gamma-I chain; kappa chain; Immunoglobulin; epithelium;
KW	malignant tumour; breast; bladder; ovary; colon; lung; brain; oesophagus;
KW	therapy.
XX	
OS	Synthetic.
XX	
PN	EP112863-A1.
XX	
PD	22-MAY-1996.
XX	
PF	15-NOV-1995; 95EP-0203126.
XX	
PR	18-NOV-1994; 94CU-0000128.
XX	
PA	(IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX	
PI	Filas EM, Mateo Del Acosta Del Rio CM, Rodriguez RP;
XX	
DR	WPI: 1996-252836/26.

XX Humanised and chimeric antibodies for EGF receptor - used in
PT diagnosis and therapy of tumours
XX
PS Claim 6; Page 12; 24pp; English.
XX
CC R99286-R96293 represent framework regions (FR) for a humanised monoclonal
CC antibody (Ab) specific for the human epidermal growth factor (EGF)
CC receptor. This Ab binds to human EGF-R, and inhibits binding of EGF to
CC the EGF-R. The humanised Ab comprises antigen binding sites (CDR's) of
CC non-human origin, and FRs of the variable and constant regions of light
CC and heavy chains of human origin. The constant heavy chain region used
CC comprises the amino acid sequence of a gamma-1 chain. The constant light
CC chain region used comprises the kappa chain of a human immunoglobulin.
CC High levels of EGF-R have been detected in malignant tumours originating
CC in the epithelium. These include breast tumours, bladder tumours,
CC ovarian tumours, colonic tumours, lung tumours, brain tumours and tumours
CC of the oesophagus. The presence of EGF-R in tumour cells is an indicator
CC of a poor prognosis (particularly in human breast cancer). The Ab can
CC therefore be used for diagnostic localisation and assessment of tumour
CC growth. The Ab can also be used in the design of a drug targeted to the
CC tumour.
CC
XX
XX Sequence 15 AA:
S0
Query Match 49.1%; Score 28; DB 17; Length 15;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 QOTAPKAP 9
Db 3 qdtpgkap 10
111111
111111
111111
RESULT 14
Y20846 Y20846 standard; Protein; 24 AA.
XX
AC Y20846;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human neurofilament-H mutant protein fragment 5.
XX
XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX MO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB00705.
XX
PR 10-APR-1997; 97US-0043163.
XX
XX (UYUT-) RIJXSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
XX (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;

DR WPI: 1998-609901/51.
DR N-PSDB: X75760.
XX
XX Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA
XX
PS Disclosure: Figure 9; 258pp; English.
XX
XX This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC use of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A.
XX
XX Sequence 24 AA:
S0
Query Match 49.1%; Score 28; DB 19; Length 24;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 QTAPEKAPT 10
Db 13 qdppgapt 20
111111
111111
111111
RESULT 15
R76042 R76042 standard; Peptide; 13 AA.
XX
AC R76042;
XX
DT 24-DEC-1995 (first entry)
XX
DE Netrin domain V peptide p78(439-451)/p75(415-427).
XX
XX Netrin domain V peptide p78(439-451)/p75(415-427).
KW Neural axon out-growth modulator; epidermal growth factor; EGF;
KW netrin-1; netrin-2; p78; p75; neurodegenerative disease.
XX
XX Gallus sp.
OS
XX
XX Key Location/Qualifiers
FT MISC-difference 4 /label- Tyr, Phe
FT FT MISC-difference 11 /label- Ile, Val
FT FT
XX
XX MO9513367-A1.
XX
PD 18-MAY-1995.
XX
XX 08-NOV-1994; 94WO-US12913.
XX
XX 12-NOV-1993; 93US-0152019.
XX
XX (REGC) UNIV CALIFORNIA.
PA (UYCO) UNIV COLUMBIA NEW YORK.

XX
PI Dodd J, Jessell T, Kennedy T, Placzek M, Serafini T,
PI Tessier-Lavigne M;
XX
DR WPI; 1995-194086/25.
XX
PT Neural axon out-growth modulators derived from EGF-like repeats of
PT netrin 1 or netrin 2 - comprise peptide(s) capable of selectively
PT increasing spinal axon out-growth or directing axon orientation
XX
PS Disclosure; Page 5; 58pp; English.
XX
CC The peptides given in R74189-200 and R76042-58 have axon outgrowth
CC and/or orienting activity and are based on domain V, domain VI
CC or the C-terminal domains of chick p78 and p75 (R74186-87).
XX
SQ Sequence 13 AA;

Query Match 47.4%; Score 27; DB 16; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 QOCTAPKAP 9
|| : ||
Db 5 qgsrpxp 13

Search completed: February 13, 2001, 13:02:02
Job time: 83 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:02:40 ; Search time 35.7 Seconds
(without alignments)
20.922 Million cell updates/sec

Title: US-09-372-036-29

Perfect score: 57

Sequence: 1 000TAPKAPTE 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 6242

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_66:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	43.9	20	2 A33878	myosin light chain
2	25	43.9	20	2 S72501	protein kinase C 1
3	24	42.1	13	2 A60458	protocatechuate 3,
4	24	42.1	15	2 S71300	ICL3 protein - Par
5	24	42.1	27	2 B60704	48k antigen - Cocc
6	23	40.4	15	2 S54712	zein Zp22/6 protei
7	23	40.4	20	2 T44453	acetyl-CoA synthet
8	23	40.4	21	2 S22875	TYA protein - yeas
9	23	40.4	22	2 I50387	c-myc protein - ch
10	23	40.4	27	2 A48989	chitinase (EC 3.2.
11	23	40.4	29	2 A39462	cholesterolin - do
12	23	40.4	29	2 T35132	hypothetical prote
13	22	38.6	13	2 S09716	25 albumin large c
14	22	38.6	16	2 S03405	hydrogenase (EC 1.
15	22	38.6	20	2 P00688	photosystem I 14.0
16	22	38.6	20	2 P00687	photosystem I 14.1
17	22	38.6	21	2 P60376	soluble immune res
18	22	38.6	23	2 F61491	seed protein wa-6
19	22	38.6	24	2 S23121	1H-3-hydroxy-4-oxo
20	22	38.6	26	2 D32248	ig kappa chain V r
21	22	38.6	27	2 E26287	apollipoprotein C-I
22	22	38.6	29	2 S07771	histone H2B-2, spe
23	22	38.6	29	2 S57225	labial protein (cl
24	22	38.6	30	2 A44010	kit-ligand (altern
25	21	36.8	9	2 PC7078	unidentified 48.7k
26	21	36.8	14	2 S11129	phosphoprotein, bo
27	21	36.8	16	2 E58503	superoxide dismuta
28	21	36.8	16	2 S38292	30k allergen - rye
29	21	36.8	20	2 PNO115	insulin-like growt

30	21	36.8	20	2 S68619	histone H3 - sea u
31	21	36.8	20	2 A34859	heliothermine - Mex
32	21	36.8	21	2 E41299	T-cell receptor al
33	21	36.8	22	2 S58433	isocitrate dehydro
34	21	36.8	22	2 D47256	kinetoplast DNA-as
35	21	36.8	24	2 S13656	matrix protein - h
36	21	36.8	27	2 I37460	histone H3 - human
37	21	36.8	27	2 A49236	omega-glialdin - el
38	21	36.8	28	2 A03356	gamma35 secalin -
39	21	36.8	29	2 S70328	hypothetical prote
40	21	36.8	30	2 S06966	major glycoprotein
41	20	35.1	11	2 S23926	cycloleucorin -
42	20	35.1	12	2 J00356	fibroblast-activat
43	20	35.1	12	2 E44787	caliMIRamide 1 -
44	20	35.1	14	2 S23376	collagen alpha cha
45	20	35.1	15	2 PC7077	ig epsilon chain C

ALIGNMENTS

RESULT 1
A33878
myosin light chain kinase, smooth muscle - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 07-Nov-1997
C:Accession: A33878
R:Ikebe, M.; Maruta, S.; Reardon, S.
J. Biol. Chem. 264, 6967-6971, 1989
A:Title: Location of the inhibitory region of smooth muscle myosin light chain kinase
A:Reference number: A33878; MUID:89214114
A:Accession: A33878
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <IKK>
C:Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homo
C:Keywords: smooth muscle

Query Match 43.9% Score 25; DB 2; Length 20;
Best Local Similarity 62.5% Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 3 OTAPKAPT 10
Db 6 KTPPKAAT 13

RESULT 2
S72501
protein kinase C inhibitor - human (fragment)
N:Alternate names: histidine triad nucleotide-binding protein
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S72501; S62623
R:Maines, M.D.; Trakheh, G.M.
Arch. Biochem. Biophys. 300, 320-326, 1993
A:Title: Purification and characterization of human biliverdin reductase.
A:Reference number: S29736; MUID:9314333
A:Accession: S72501
A:Molecule type: protein
A:Residues: 1-20 <MAI>
A>Note: this protein was identified as biliverdin reductase; the identification is qu
Eur. J. Biochem. 235, 372-381, 1996
A:Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati
A:Reference number: S62622; MUID:96202961
A:Accession: S62623
A:Molecule type: protein
A:Residues: 1-20 <MAW>
C:Superfamily: protein kinase C inhibitor; histidine triad homology
C:Keywords: homodimer; protein kinase inhibitor; zinc

Query Match 43.9%; Score 25; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 APPAPT 10.
:|:|:|
Db 8 SPQAPT 13

RESULT 3
A60458
protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain GU2)

N:Alternate names: protocatechuate oxygenase
C:Species: Moraxella sp.
C:Date: 20-Feb-1993 #sequence_rev1sion 20-Feb-1993 #text_change 07-May-1999

C:Accession: A60458
R:Sterjades, R.; Belmont, J.
Appl. Environ. Microbiol. 55, 340-347, 1989

A:Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Morax

A:Reference number: A60458; MUID:89245845
C:Accession: A60458

A:Molecule type: protein
A:Residues: 1-13 <STRE>

A:Note: Two forms P and G of the alpha subunit yielded identical amino terminal sequence
C:Keywords: Iron; oxidoreductase

Query Match 42.1%; Score 24; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 QTAAPAPT 10
:|:|:|
Db 3 RTAKAPAPT 10

RESULT 4
S71300
ICL3 protein - Parametium tetraurelia (fragment)

C:Species: Parametium tetraurelia
C:Date: 11-Mar-1998 #sequence_rev1sion 17-Apr-1998 #text_change 07-Dec-1999

C:Accession: S71300
R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996

A:Title: Characterization of centrin genes in Parametium.
A:Reference number: S71296; MUID:96248429

A:Accession: S71300
A:Molecule type: protein

A:Residues: 1-15 <MAD>
A:Experimental source: strain d4-2

C:Genetics:
A:Genetic code: SGCS

Query Match 42.1%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 QOTAPKAP 9
:|:|:|
Db 6 QKNXPKAP 13

RESULT 5
B60704
48k antigen - Coccidioides immitis (fragment)

C:Species: Coccidioides immitis
C:Date: 28-Apr-1993 #sequence_rev1sion 28-Apr-1993 #text_change 10-May-1996

C:Accession: B60704
R:Resnick, S.; Zimmer, B.; Pappagianis, D.; Eakin, A.; McKerrow, J.
J. Clin. Microbiol. 28, 385-388, 1990

A:Title: Purification and amino-terminal sequence analysis of the complement-fixing and

A:Reference number: A60704; MUID:90187015
A:Accession: B60704
A:Molecule type: protein
A:Residues: 1-27 <RES>
C:Superfamily: Streptomyces chitinase chl40

Query Match 42.1%; Score 24; DB 2; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 PKAPTE 11
:|:|:|
Db 5 PEAPAE 10

RESULT 6
S54712
zein 2p22/6 protein - maize

C:Species: Zea mays (maize)
C:Date: 23-Aug-1995 #sequence_rev1sion 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: S54712
R:Chaudhuri, S.; Messing, J.

Mol. Gen. Genet. 246, 707-715, 1995
A:Title: RFLP mapping of the maize d2r1 locus, which regulates methionine-rich 10 kDa

A:Reference number: S54712; MUID:95206245
A:Accession: S54712

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <CHA>

Query Match 40.4%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QOOTAPKA 8
:|:|:|
Db 5 QOSTAPPA 12

RESULT 7
T44453
acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa
C:Date: 21-Jan-2000 #sequence_rev1sion 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T44453
R:Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.

J. Bacteriol. 180, 5559-5566, 1998
A:Title: Molecular characterization and regulation of an operon encoding a system for

A:Reference number: Z22777; MUID:99008987
A:Accession: T44453
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-20 <NTS>

A:Cross-references: EMBL:AF012537; MUID:92668593; PIDN:AACT1069.1; PID:92668594
A:Experimental source: strain PA01

Query Match 40.4%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 TAPKAPT 10
:|:|:|
Db 8 TSPPLPT 14

RESULT 8
S22875
TyA protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty3 (fragment)

C:Species: Saccharomyces cerevisiae
C:Date: 04-Dec-1992 #sequence_rev1sion 04-Dec-1992 #text_change 25-Apr-1997

C:Accession: S22875
R:Clark, D.J.; Bilanchone, V.W.; Haywood, L.J.; Dildine, S.L.; Sandmeyer, S.B.
J. Biol. Chem. 263, 1413-1423, 1988
A:Title: A yeast sigma composite element, Ty3, has properties of a retrotransposon.
A:Reference number: S22875; MUID:88087281

A:Accession: S22875
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-21 <CL>
A:Cross-references: EMBL:M18353
A:Experimental source: strain AB972
C:Genetics:
A:Mobile element: retrotransposon Ty3

Query Match 40.4%; Score 23; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 PKAPTE 11
|||
Db 14 PKLPVE 19

RESULT 9
150387
c-myc protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: 150387
R:Westaway, D.; Payne, G.; Varnus, H.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 843-847, 1984
A:Title: Proviral deletions and oncogene base-substitutions in insertionally mutagenized
A:Reference number: 150387; MUID:84144799
A:Accession: 150387
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <MES>
A:Cross-references: GB:K01440; NID:g212357; PIDN:AAA48964.1; PID:g212358

Query Match 40.4%; Score 23; DB 2; Length 24;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 PKAPTE 11
|||
Db 2 PPAPSE 7

RESULT 10
A48989
chitinase (EC 3.2.1.14) - Alteromonas (fragment)
C:Species: Alteromonas
C:Date: 21-Jan-1994 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C:Accession: A48989
R:Tsujiho, H.; Yoshida, Y.; Miyamoto, K.; Imada, C.; Okami, Y.; Inamori, Y.
Can. J. Microbiol. 38, 891-897, 1992
A:Title: Purification, properties, and partial amino acid sequence of chitinase from a
A:Reference number: A48989; MUID:9309552.
A:Contents: 0-7
A:Accession: A48989
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-27 <TSU>
A:Note: sequence extracted from NCBI backbone (NCBIP:121209)
C:Keywords: glycosidase; hydrolase

Query Match 40.4%; Score 23; DB 2; Length 27;
Best Local Similarity 66.7%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 APKAPT 10
|||
Db 1 APSTPT 6

RESULT 11
A39462
cholesterolkinin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 12-Apr-1995
C:Accession: A39462
R:Reeve Jr., J.R.; Eysselehn, V.E.; Eberlein, G.A.; Chew, P.; Ho, F.J.; Huebner, V.D.
J. Biol. Chem. 266, 13770-13776, 1991
A:Title: Characterization of canine intestinal cholecystokinin-58 lacking its carboxy
A:Reference number: A39462; MUID:91310654
A:Accession: A39462
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <REE>
C:Superfamily: gastrin

Query Match 40.4%; Score 23; DB 2; Length 29;
Best Local Similarity 62.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 OTAPKAPT 10
|||
Db 22 OQARKAPS 29

RESULT 12
T35132
hypothetical protein SC4H8.01 SC4H8.01 - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35132
R:Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL data library, December 1997
A:Reference number: Z21569
A:Accession: T35132
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-29 <HAR>
A:Cross-references: EMBL:AL020958; PIDN:CAI5868.1; GSPDB:GN00070; SCOEDB:SC4H8.01
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC4H8.01

Query Match 40.4%; Score 23; DB 2; Length 29;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 OTAPKAPT 9
|||
Db 17 QDAPREP 23

RESULT 13
S09716
2S albumin large chain (1 and 2) nrl - rape (fragments)
N:Alternate names: 2S albumin large chain nrl
C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S09716; S09718; S09717
R:Moysalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-turns as structural motifs for the proteolytic processing of seed prote
A:Reference number: S09720; MUID:90242974
A:Accession: S09716
A:Molecule type: protein
A:Residues: 1-9;10-13 <MON>

A:Experimental source: seed
 A:Note: 3-Ser was also found
 A:Accession: S09718
 A:Molecule type: protein
 A:Residues: 1-9:10-13 <MO2>
 A:Experimental source: seed
 A:Accession: S09717
 A:Molecule type: protein
 A:Residues: 1-9:10-13 <MO3>
 A:Experimental source: seed

Query Match 38.6%; Score 22; DB 2; Length 13;
 Best Local Similarity 44.4%; Pred. No. 5e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 QOTAPKAPT 10
 :| | | :
 DB 5 QQRPPGPGS 13

RESULT 14

S03405
 hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)
 C:Species: Alcaligenes eutrophus
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Sep-1998
 C:Accession: S03405
 R:Lorenz, B.; Schneider, K.; Kratzin, H.; Schlegel, H.G.
 Blochim. Biophys. Acta 995, 1-9, 1989
 A>Title: Immunological comparison of subunits isolated from various hydrogenases of aerob
 A:Reference number: S03404; MID:89166525
 A:Accession: S03405
 A:Molecule type: protein
 A:Residues: 1-16 <LOR>
 A:Experimental source: strain H16, DMS 541
 C:Superfamily: hydrogenase (Nlfe) small chain
 C:Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein; ni

Query Match 38.6%; Score 22; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 6.1e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 QOTAPKAP 9
 :| | | :
 DB 2 ETKKPRP 8

RESULT 15

PQ0688
 photosystem I 14.0K E4 chain - common tobacco (fragment)
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
 C:Accession: PQ0688
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
 Plant Physiol. 102, 1259-1267, 1993
 A>Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are a
 A:Reference number: PQ0667; MID:94105345
 A:Accession: PQ0688
 A:Molecule type: protein
 A:Residues: 1-20 <O8O>
 C:Keywords: chloroplast; photosynthesis; photosystem I

Query Match 38.6%; Score 22; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 7.7e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 QOTAPKAPT 10
 :| | | :
 DB 2 EDAAPPAPT 10

THIS PAGE BLANK (USPTO)

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:06:53 ; Search time 20.83 Seconds
(without alignments)
17.054 Million cell updates/sec

Title: US-09-372-036-29
Perfect score: 57
Sequence: 1 000TAPKAPTE 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues
Total number of hits satisfying chosen parameters: 1785

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwlssProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	38.6	29	1 H2B2_ECHES	P13282 echinus esc
2	21	36.8	20	1 CUDP_VERCH	P00406 verticillium
3	21	36.8	20	1 HELT_HELHO	P46653 heloderma h
4	21	36.8	28	1 GDO_TRIHO	P02865 triticum mo
5	20	35.1	12	1 FARI_CALVO	P18659 calliphora
6	20	35.1	15	1 UNO1_PINDS	P11066 pinus pinas
7	20	35.1	17	1 RM35_YEAST	P36550 saccharomyc
8	20	35.1	20	1 M117_BOVIN	P35451 bos taurus
9	20	35.1	25	1 H2B1_ECHES	P13281 echinus esc
10	20	35.1	27	1 L52_ADE07	P05663 human adeno
11	20	35.1	28	1 HORC_HORSP	P02864 hordeum spo
12	19	33.3	10	1 BPP_VIPAS	P13351 vipera aspl
13	19	33.3	18	1 F1BB_AANPL	P12802 anas platyr
14	19	33.3	19	1 PSAE_CUCSA	P42047 cucumis sat
15	19	33.3	23	1 TRYL_RAT	P27436 rattus norv
16	19	33.3	27	1 LIPS_BOVIN	P16386 bos taurus
17	19	33.3	27	1 PPS1_DROFU	P01372 drosophila
18	19	33.3	29	1 PRO1_DACGL	P18689 dactylis gl
19	18	31.6	7	1 UPO4_MOUSE	P38642 mus musculu
20	18	31.6	10	1 AL19_CARMA	P81822 carcinus ma
21	18	31.6	10	1 SPCRC_RABIT	P56233 oryctolagus
22	18	31.6	11	1 BPPB_AGRHA	P01021 agkistrodon
23	18	31.6	12	1 TALO_TREME	P01371 tremella me
24	18	31.6	14	1 TAT_HV1W2	P12509 human immun
25	18	31.6	14	1 TAT_HV1W2	P12511 human immun
26	18	31.6	15	1 ATP2_SPTOL	P80083 spinacia ol
27	18	31.6	15	1 SODM_STRGR	P80733 streptomyc
28	18	31.6	17	1 A45K_MYCBO	P80069 mycobacteri
29	18	31.6	19	1 ATPB_CANFA	P99504 canis fami
30	18	31.6	20	1 YOAH_KLEAE	P56506 klebsiella
31	18	31.6	21	1 AROF_STRCO	P80574 streptomyc
32	18	31.6	23	1 PRO3_DACGL	P18650 dactylis gl
33	18	31.6	27	1 IPPD_MOUSE	P060829 mus musculu

34	18	31.6	29	1 TAT_HV1W2	P12510 human immun
35	18	31.6	30	1 ACB1_DIGIA	P81624 digitalis 1
36	17.5	30.7	19	1 TRP3_LEUMA	P81735 leucophaea
37	17	29.8	10	1 COXM_RAT	P80431 rattus norv
38	17	29.8	10	1 COXO_SHEEP	P80337 ovis aries
39	17	29.8	15	1 UC30_MAIZE	P80636 zea mays (m
40	17	29.8	16	1 RBL_CAPAN	P27063 capsicum an
41	17	29.8	16	1 RBL_CUCSA	P27064 cucumis sat
42	17	29.8	16	1 RBL_VIGSI	P27067 vigna sinen
43	17	29.8	17	1 TRP2_LEUMA	P81733 leucophaea
44	17	29.8	18	1 DRPH_PANBO	P01209 pendulus bo
45	17	29.8	19	1 UKAL_HUMAN	P31940 homo sapien

ALIGNMENTS

RESULT 1					
H2B2_ECHES	STANDARD:	PRT:	29 AA.		
ID H2B2_ECHES					
AC P13282;					
DT 01-JAN-1990 (Rel. 13, Created)					
DT 01-FEB-1991 (Rel. 17, Last sequence update)					
DT 30-MAY-2000 (Rel. 39, Last annotation update)					
DE HISTONE H2B.2, SPERM (FRAGMENT).					
OS Echinus esculentus (Sea urchin).					
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;					
OC Echinoidae; Euechinoidae; Echinacea; Echinidae; Echinidae; Echinus.					
RN [1]					
RP SEQUENCE.					
RX MEDLINE=90126812; PubMed=2298202;					
RA Hill C.S., Thomas J.O.;					
RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-					
terminal tail of H2B interacts with linker DNA.";					
RL Eur. J. Biochem. 187:145-153(1990).					
CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF					
CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.					
CC -1- SUBCELLULAR LOCATION: NUCLEAR.					
CC -1- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.					
DR PIR: S07771: S07771.					
DR INTERPRO: IPR000558; -					
DR PROSITE: PS00357; HISTONE_H2B; PARTIAL.					
KW Nucleolar protein; Chromosomal protein; Nucleosome core; DNA-binding;					
KW Multigene family.					
FT NON TER 29					
SO SEQUENCE 29 AA; 2989 MW; 82EBE7137332E74B CRC64;					
Query: Match 38.6%; Score 22; DB 1; Length 29;					
Best local similarity 50.0%; Pred. No. 5.2e+02;					
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;					
Oy: 6 PKAPPE 11					
Db: 1 PKSPSK 6					
RESULT 2					
CUDP_VERCH	STANDARD:	PRT:	20 AA.		
ID CUDP_VERCH					
AC P80406;					
DT 01-NOV-1995 (Rel. 32, Created)					
DT 01-NOV-1995 (Rel. 32, Last sequence update)					
DT 15-DEC-1998 (Rel. 37, Last annotation update)					
DE CUTICLE-DEGRADING PROTEASE-LIKE PROTEIN (EC 3.4.21.-) (CHYMOELASTASE)					
OS Verticillium chlamydosporium.					
OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Diketeterospora.					
RN [1]					
RC STRAIN=VC10;					
RA MEDLINE=95247009; PubMed=7729666;					
RA Segers R., Butt T.M., Keen J.N., Kerry B.R., Peberdy J.F.;					

RT "The subtilisins of the invertebrate mycopathogens *Verticillium*
 RT *chlamydosporium* and *Metarhizium anisopliae* are serologically and
 RT functionally related."
 RL FEMS Microbiol. Lett. 126:227-231(1995).
 CC -1- FUNCTION: CAPABLE OF BREACHING THE INSECT CUTICLE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
 CC SUBTILASE FAMILY.
 DR MEROPS: S08.056; .
 DR INTERPRO: IPR000209; .
 DR PROSITE: PS00136; SUBTILASE_ASP: PARTIAL.
 DR PROSITE: PS00137; SUBTILASE_LIS: PARTIAL.
 DR PROSITE: PS00138; SUBTILASE_SER: PARTIAL.
 KM Hydrolyase; serine protease.
 FT NON_TER 20
 FT SEQUENCE 20 AA; 2113 MW; 2674BC2F7729B19 CRC64;

Query Match 36.8%; Score 21; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 5.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOQTAP 6
 DB 4 EQOGAP 9

RESULT 3
 HELT_HELHO
 ID HELT_HELHO STANDARD; PRT; 20 AA.
 AC P46693;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HELOHERMINE (FRAGMENT).
 OS Heloderma horridum horridum (Mexican beaded lizard).
 OS Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Lepidossauria; Squamata; Scleroglossa; Anguilliformia; Helodermatidae;
 OC Heloderma.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM;
 RX MEDLINE-90260878; PubMed-1693019;
 RA Mochizuki-Morales J., Martin B.M., Posaani L.D.;
 RT "Isolation and characterization of helohermine, a novel toxin from
 RT *Heloderma horridum horridum* (Mexican beaded lizard) venom."
 RL Toxicon 28:299-309(1990).
 CC -1- FUNCTION: TOXIC TO WICE; INDUCES LETHARGY, PARTIAL PARALYSIS OF
 CC REAR LIMBS AND LOWERING OF BODY TEMPERATURE, SUGGESTING THAT IT
 CC MIGHT BE A HYPOTHERMIC TOXIN.
 CC -1- MISCELLANEOUS: THE COMPLETE PROTEIN HAS AN APPARENT MW OF 25 KDA
 CC AND A PI OF 6.8.
 DR PIR: A34859; A34859.
 KM Toxin.
 FT NON_TER 20
 FT SEQUENCE 20 AA; 2156 MW; 91D62B36F7BAF940 CRC64;

Query Match 36.8%; Score 21; DB 1; Length 20;
 Best Local Similarity 42.9%; Pred. No. 5.3e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 QOTAPAP 9
 DB 1 EASPKLP 7

RESULT 4
 GDO_TRIMO
 ID GDO_TRIMO STANDARD; PRT; 28 AA.
 AC P02865;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE OMEGA-GLUTADIN (FRAGMENT).
 OS Triticum monococcum (Einkorn wheat) (Small spelt).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 RN [1]
 RP SEQUENCE.
 RA Shewry P.R., Autran J.-C., Nimmo C.C., Lew E.J.-L., Kasarda D.D.;
 RT "N-terminal amino acid sequence homology of storage protein components
 RT from barley and a diploid wheat."
 RL Nature 286:520-522(1980).
 DR PIR: A03356; A03356.
 KM Seed storage protein.
 FT NON_TER 28
 FT SEQUENCE 28 AA; 3343 MW; EA36C84E893FAA7 CRC64;

Query Match 36.8%; Score 21; DB 1; Length 28;
 Best Local Similarity 50.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 QOTAPAP 9
 DB 15 QOLYPOQ 22

RESULT 5
 FART_CALVO
 ID FART_CALVO STANDARD; PRT; 12 AA.
 AC P41869;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CALLIMIRFAMIDE 1.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Calliphoridae; Calliphora.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-THORACIC GANGLION;
 RX MEDLINE-92196111; PubMed-1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliphramide) from the blowfly
 RT *Calliphora vomitoria*."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR: E44787; E44787.
 DR Neuuropeptide; Amidation.
 KM MOD_RES 12
 FT MOD_RES 12
 FT SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 35.1%; Score 20; DB 1; Length 12;
 Best Local Similarity 42.9%; Pred. No. 4.8e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 APKAPTE 11
 DB 1 APNQPSD 7

RESULT 6
 UNOL_PINPS
 ID UNOL_PINPS STANDARD; PRT; 15 AA.
 AC P81106;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (S1247/S1248) (N150/N151)

DE (FRAGMENT).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Pinus.
RN [1]
RP SEQUENCE.
RA TISSUE-NEEDLE:
RC Plomion C., Costa P., Bahrman N., Frigerio J.M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue. In
RT a haploid-based genetic map";
RL Silvine Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE-NEEDLE:
RX MEDLINE-99274088; PubMed-10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 62 KDA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match 35.18; Score 20; DB 1; Length 15;
Best Local Similarity 36.48; Pred. No. 6e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 QOQTAPKAPTE 11
DB 3 EQITQPSATND 13

RESULT 7
RM35_YEAST
ID RM35_YEAST STANDARD; PRT; 17 AA.
AC P36530;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L35 (YML35) (FRAGMENT).
DE MRPL35.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE.
RX MEDLINE-91285106; PubMed-2060626;
RA Grohmann L., Gracko H.-R., Kruff V., Choll T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria";
RL FEBS Lett. 284:51-56(1991).
DR PIR: S17274; S17274
DR SGD: S0002730; MRPL35.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1826 MW; 6CE89CB415483EE8 CRC64;

Query Match 35.18; Score 20; DB 1; Length 17;
Best Local Similarity 37.58; Pred. No. 6.8e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 TAPKAPTE 11
DB 4 TSERLPTD 11

RESULT 8
M17_BOVIN
ID M17_BOVIN STANDARD; PRT; 20 AA.
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 KDA MILK GLYCOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE-MILK:
RX MEDLINE-93308294; PubMed-8320368;
RA Sorensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
RT the protease peptone fraction of bovine milk";
RL J. Dairy Res. 60:189-197(1993).
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 35.18; Score 20; DB 1; Length 20;
Best Local Similarity 50.08; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 QOQTAPKAP 9
DB 6 OSQNPKLP 13

RESULT 9
H2B1_ECHES
ID H2B1_ECHES STANDARD; PRT; 25 AA.
AC P13281;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HISTONE H2B.1, SPERM (FRAGMENT).
OS Echinus esculentus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinodermata; Echinacea; Echinoidae; Echinidae; Echinus.
RN [1]
RP SEQUENCE.
RX MEDLINE-90126812; PubMed-2298202;
RA Hill C.S., Thomas J.O.;
RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-
RT terminal tail of H2B interacts with linker DNA";
RL Eur. J. Biochem. 187:145-153(1990).
CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4, WHICH WRAP APPROXIMATELY 146 BP OF DNA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
DR PIR: S07770; S07770.
DR INTERPRO: IPR000558;
DR PROSITE: PS00357; HISTONE_H2B; PARTIAL.
KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
KW Multigene family.
FT NON_TER 25
FT NON_TER 25
SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D73A3A9EC CRC64;

Query Match 35.18; Score 20; DB 1; Length 25;
Best Local Similarity 27.38; Pred. No. 1e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 QOQTAPKAPTE 11

DB 3 QKSPTRKSPK 13

RESULT 10
L52_ADE07 STANDARD: PRT: 27 AA.
ID L52_ADE07
AC P05663;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LATE L1 52 KDA PROTEIN (FRAGMENT).
OS Human adenovirus type 7.
NC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COMEN:
RX MEDLINE=83183660; PubMed=6301944;
RA Engler J.A., Hoppe M.S., van Bree M.P.;
RT "The nucleotide sequence of the genes encoded in early region 2b of
human adenovirus type 7.";
RL Gene 21:145-159(1983).
CC -1- FUNCTION: INVOLVED IN VIRION ASSEMBLY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X03000; CAA26776.1; -
CC DR LATE PROTEIN.
CC FT NON_TER 27 27
CC SEQUENCE 27 AA: 3108 MW: 55A8288B117B533 CRC64;

Query Match

Best Local Similarity 35.1%; Score 20; DB 1; Length 27;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QQTAP 6
DB 11 QOQAP 15

RESULT 11
HORC_HORSP STANDARD: PRT: 28 AA.
ID HORC_HORSP
AC P02864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE C-HORDEIN (FRAGMENT).
OS Hordeum spontaneum (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
RN [1]
RP SEQUENCE.
RA Shewry P.R., Autran J.-C., Nimmo C.C., Lew E.J.-L., Kasarda D.D.;
RT "N-terminal amino acid sequence homology of storage protein components
from barley and a diploid wheat.";
RL Nature 286:520-522(1980).
CC -1- FUNCTION: SULFUR-POOR SEED STORAGE PROTEIN.
CC -1- TISSUE SPECIFICITY: DEVELOPING ENDOSPERM.
CC PIR: A03355; A03355.
KW Seed storage protein; Multigene family.
FT NON_TER 28 28
CC SEQUENCE 28 AA: 3333 MW: 8DBA2DF2494775AA CRC64;

Query Match

35.1%; Score 20; DB 1; Length 28;

Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QQTAPKAP 9
DB 19 QOQPPQNP 26

RESULT 12
BPP_VIPAS STANDARD: PRT: 10 AA.
ID BPP_VIPAS
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Vipera aspis (aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Vipera.
RN [1]
RP SEQUENCE.
RC TISSUE-VENOM.
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
CC PIR: A60377; XASNPC.
CC DR HYPOTENSIVE agent; Venom.
CC FT MOD_RES 1 1
CC SEQUENCE 10 AA: 1062 MW: 3BA827C327686773 CRC64;

Query Match

Best Local Similarity 73.3%; Score 19; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PKAP 9
DB 6 PKVP 9

RESULT 13
FIBB_ANAPL STANDARD: PRT: 18 AA.
ID FIBB_ANAPL
AC P12802;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIBRINOPEPTIDE B.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
RN [1]
RP SEQUENCE.
RA MEDLINE=85168193; PubMed=3983613;
RX Min Y., Ping Z., Yaoshi Z.;
RT "Purification and primary structures of duck fibrinopeptides A and
B.";
RL Sci. Sin., B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA

CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR: JP0102; JP0102.
 DR INTERPRO: IPR002181; .
 DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KM Blood coagulation; Plasma; Sulfation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 6 6 SULFATATION.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2028 MW; B0F15E7768F8A1F9 CRC64;

OY 2 QO7APKA 8
 Db 11 ESTYPEA 17

RESULT 14
 PSAC_CUCSA STANDARD: PRT: 19 AA.
 AC P42047;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 19.5 KDA
 DE PROTEIN) (PSI-E) (PS I SUBUNIT 6) (FRAGMENT).
 GN PSAC.
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Cucurbitales; Cucurbitaceae; Cucumis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-COTYLEDON;
 RX MEDLINE-91355209; PubMed-1883835;
 RA Iwasaki Y., Ishikawa H., Hibino T., Takebe T.;
 RT "Characterization of genes that encode subunits of cucumber PS I
 RT complex by N-terminal sequencing";
 RL Biochim. Biophys. Acta 1059:141-148(1991).
 CC -1- FUNCTION: MAY FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-
 CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE PSAC FAMILY.
 KM Photosynthesis; Photosystem I; Chloroplast; Thylakoid membrane.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 1810 MW; A93E8BDD089FB738 CRC64;

Query Match 33.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TAPKA 8
 Db 11 TAPKA 15

RESULT 15
 TRYL_RAT STANDARD: PRT: 23 AA.
 ID TRYL_RAT
 AC P27436;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TRYPTASE-LIKE PROTEASE (EC 3.4.21.59) (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]

RP SEQUENCE.
 RC TISSUE-BREAST CARCINOMA;
 RX MEDLINE-92231826; PubMed-1314562;
 RA Eto I., Grubbs C.J.;
 RT "Separation, purification and N-terminal sequence analysis of a novel
 RT leupeptin-sensitive serine endopeptidase present in chemically
 RT induced rat mammary tumour";
 RL Biochem. J. 283:209-216(1992).
 CC -1- FUNCTION: THIS PROTEASE MAY BE INVOLVED IN THE PROCESS OF TUMOR
 CC INVASION AND METASTASIS.
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-1-, LYS-1-, BUT
 CC WITH MORE RESTRICTED SPECIFICITY THAN TRYPSIN.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: PRESENT IN MAMMARY TUMORS AT LEVELS AT LEAST
 CC 20 TIMES HIGHER THAN THOSE FOUND IN NORMAL MAMMARY TISSUE.
 CC -1- INDUCTION: BY INDUCERS OF MAMMARY TUMORS, LIKE N-METHYL-N-
 CC NITROSUREA.
 CC -1- PTM: GLYCOSYLATED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. STRONGEST TO OTHER TRYPTASES.
 DR PIR: S21275; S21275.
 DR HSSP: P20231; 1AAO.
 DR MEROPS: S01.143; .
 DR INTERPRO: IPR001254; .
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KM Hydrolyase; Serine protease; Glycoprotein; Multigene family.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2422 MW; 9597884E65FF02D3 CRC64;

Query Match 33.3%; Score 19; DB 1; Length 23;
 Best Local Similarity 27.3%; Pred. No. 1.4e+03;
 Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QO7APKA PTE 11
 Db 5 QEASGNKKXPVQ 15

Search completed: February 13, 2001, 13:06:53
 Job time: 285 sec

THIS PAGE BLANK (USPTO)

```

RESULT 2
P81149 PRELIMINARY; PRT: 23 AA.
AC P81149;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE CYTOCHROME C3 (FRAGMENT).
OC Desulfovibrio vulgaris.
OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
OX NCBI_TaxID=81;
RN [1]
RP SEQUENCE.
RX MEDLINE=93272123; PubMed=8388770;
  Kwon D.Y., Veddick T.S., McCue A.F., Gervetz D.;
  "Rapid comparison of the cytochrome c3 gene from nine strains of
  Desulfovibrio vulgaris using polymerase chain reaction
  amplification.";
RT Can. J. Microbiol. 39:402-411(1993).
RL -1- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
  PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
  DEHYDROGENASE TO FERREDOXIN.
CC -1- PTM: BINDS FOUR NONPARALLEL HEME GROUPS PER MOLECULE.
CC -1- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
DR HSSP: P00132; 2CDV.
KM Electron transport; Sulfate respiration; Heme.
FT METAL 13 13 IRON (HEME 1 AXIAL LIGAND) (BY
FT METAL 16 16 SIMILARITY).
FT NON_TER 23 23 IRON (HEME 3 AXIAL LIGAND) (BY
FT SEQUENCE 23 AA; 2477 MW; 1114D6A4C22FAD6B CRC64;

```

```

Query Match 50.9%; Score 29; DB 2; Length 23;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 5 APRKAPTE 11
DB 2 APRKAPAD 8

RESULT 3
O9OUY8 PRELIMINARY; PRT: 16 AA.
AC O9OUY8;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE HISTONE H1 (FRAGMENT).
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniala; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE.
RX MEDLINE=96070893; PubMed=7499230;
  Gurley L.R., Valdez J.G., Buchanan J.S.;
  "Characterization of the mitotic specific phosphorylation site of
  histone H1. Absence of a consensus sequence for the p34cdc2/cyclin B
  kinase.";
RT J. Biol. Chem. 270:27653-27660(1995).
RL SEQUENCE 16 AA; 1479 MW; 75EB4B8737288C8A CRC64;

```

```

Query Match 49.1%; Score 28; DB 11; Length 16;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 3 QTAPKAPTE 9
DB 2 ETAPAP 8

RESULT 4
O9TRW4 PRELIMINARY; PRT: 20 AA.
AC O9TRW4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 25 KDA PROTEIN P25, PEPTIDE F5A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
  Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
  Shiratsuchi A., Uchida T., Imahori K.;
  "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
  Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
RT FEBS Lett. 289:37-43(1991).
RL SEQUENCE 20 AA; 2032 MW; 4AADB849A6416897 CRC64;

```

```

Query Match 49.1%; Score 28; DB 6; Length 20;
Best Local Similarity 55.6%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 3 QTAPKAPTE 11
DB 11 KTPKSPGE 19

RESULT 5
O9TRW3 PRELIMINARY; PRT: 27 AA.
AC O9TRW3;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 25 KDA PROTEIN P25, PEPTIDE F5B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
  Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
  Shiratsuchi A., Uchida T., Imahori K.;
  "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
  Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
RT FEBS Lett. 289:37-43(1991).
RL SEQUENCE 27 AA; 2787 MW; 8DCEFD1811407B23 CRC64;

```

```

Query Match 49.1%; Score 28; DB 6; Length 27;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 3 QTAPKAPTE 11
DB 11 KTPKSPGE 19

RESULT 6

```

069350
ID 069350 PRELIMINARY; PRT; 22 AA.
AC 069350;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
DE 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DS HSV-2 (333) GLYCOPROTEIN C GENE FRAGMENT (0.640 MU) (FRAGMENT).
OS Herpes simplex virus (type 2).
OC Alphaviruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae: Simplexvirus.
OX NCBI_TaxID=10310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85033906; PubMed=6092683;
RA Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,
Wagner E.K.;
RT "Herpes simplex virus types 1 and 2 homology in the region between
RT 0.58 and 0.68 map units."
RL J. Virol. 52:615-623(1984).
DR EMBL: K03358; AAA45838.1; -.
FT NON_TER 1 1
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2527 MW; 427404EA94AB3B84 CRC64;

Query Match 47.4%; Score 27; DB 12; Length 22;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 QQTAPKAPTE 11
: : : : :
Db 11 QPFRDPTE 19

RESULT 7
ID 09S8P6 PRELIMINARY; PRT; 21 AA.
AC 09S8P6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE FERREDOXIN-NADP(+)-OXIDOREDUCTASE (FRAGMENT).
OS Pisum sativum (Garden pea).
OC Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eurosids I;
OC Fabales: Fabaceae; Papilionoideae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE.
RX MEDLINE=94115178; PubMed=8286947;
RA Bowers C.G., Dunbar B., Emes M.J.;
RT "The purification and properties of ferredoxin-NADP(+)-oxidoreductase
RT from roots of Pisum sativum L."
RL Protein Expr. Purif. 4:512-518(1993).
SQ SEQUENCE 21 AA; 2266 MW; F51900DA268EFD5FF CRC64;

Query Match 45.6%; Score 26; DB 10; Length 21;
Best Local Similarity 45.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 QOQTAPKAPTE 11
: : : : :
Db 3 QOASVPKATVE 13

RESULT 8
ID 09R4Z4 PRELIMINARY; PRT; 20 AA.
AC 09R4Z4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE AMBIENT-TEMPERATURE FIMBRIA; ATF.
OS Proteus mirabilis.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE.
RX MEDLINE=94222573; PubMed=7909538;
RA Massad G., Bahrani F.R., Mobley H.L.;
RT "Proteus mirabilis fimbriae: identification, isolation, and
RT characterization of a new ambient-temperature fimbria."
RL Infect. Immun. 62:1989-1994(1994).
SQ SEQUENCE 20 AA; 2017 MW; B2FC481003883AE2 CRC64;

Query Match 43.9%; Score 25; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 QOQTAPKAPTE 11
: : : : :
Db 1 EXTGTAPTE 10

RESULT 9
ID 085736 PRELIMINARY; PRT; 21 AA.
AC 085736;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GAGP58 (FRAGMENT).
OS Murine sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
OX NCBI_TaxID=11802;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85108156; PubMed=2982040;
RA Nash M.A., Brizzard B.L., Wong J.L., Murphy E.C. Jr.;
RT "Murine sarcoma virus ts110 RNA transcripts: origin from a single
RT proviral DNA and sequence of the gag-mos junctions in both the
RT precursor and spliced viral RNAs."
RL J. Virol. 53:624-633(1985).
DR EMBL: K02857; AAA46577.1; -.
FT NON_TER 1 1
SQ SEQUENCE 21 AA; 2589 MW; 439B3EB8A51A08FC CRC64;

Query Match 43.9%; Score 25; DB 12; Length 21;
Best Local Similarity 44.4%; Pred. No. 3e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 QOQTAPKAP 9
: : : : :
Db 5 EERHAPKLP 13

RESULT 10
ID 09UKS2 PRELIMINARY; PRT; 29 AA.
AC 09UKS2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE NUP98-RAP1GDS1 FUSION PROTEIN TYPE 1 (FRAGMENT).
GN NRG.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
OC Mammalia: Eutheria: Primates: Catarrhini: Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hussey D.J., Nicola M., Moore S., Dobrovic A.;

RT "The (4;11)(q21;p15) translocation fuses the NUP98 and RAPIGDS1 genes
 RT and is recurrent in T cell acute lymphocytic leukemia."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF133331; AAD54075.1; -
 FT NON_TER 1 1
 FT SEQUENCE 29 AA; 2971 MW; 3A6F7048FB324B01 CRC64;

Query Match 43.9%; Score 25; DB 4; Length 29;
 Best Local Similarity 57.1%; Pred. No. 4.1e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 APRAPTE 11
 DB 9 APOAPVD 15

RESULT 11
 ID 018764 PRELIMINARY; PRT; 21 AA.
 AC 018764;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR, BETA 4 SUBUNIT (FRAGMENT).
 GN CHRNBA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98161940; PubMed=9501320;
 RT Tammen I.;
 RA "Genetic mapping of CHRN3 and CHRN4 to pig chromosome 7 extends the
 RT syntenic conservation with human chromosome 15 and mouse chromosome
 RT 9."
 RL Mamm. Genome 9:263-264(1998).
 DR EMBL: AF007797; AAC13376.1; -
 FT NON_TER 1 1
 FT SEQUENCE 21 AA; 2196 MW; EA98A064013C0FFD CRC64;

Query Match 42.1%; Score 24; DB 6; Length 21;
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 APRAP 9
 DB 14 APRSP 18

RESULT 12
 ID 090EVO PRELIMINARY; PRT; 22 AA.
 AC 090EVO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HISTONE DEACETYLASE 3 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98028756; PubMed=9360932;
 RA Lynch E.D., Lee M.K., Morrow J.E., Welcsh P.D., Leon P.E., King M.C.;
 RT "Nonsyndromic deafness DFNA1 associated with mutation of a human
 RT homolog of the Drosophila gene diaphanous."
 RL Science 278:1315-1318(1997).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98125547; PubMed=9464271;
 RA Dangond F., Hafner D.A., Tong J.K., Randall J., Kojima R., Utku N.,
 RA Guillan S.R.;
 RT "Differential display cloning of a novel human histone deacetylase
 RT (HDAC3) cDNA from PHA-activated immune cells."
 RL Biochem. Biophys. Res. Commun. 242:648-652(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lynch E.D., Lee M.K., King M.-C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF053139; AAC08352.1; -
 FT NON_TER 1 1
 FT SEQUENCE 22 AA; 2536 MW; 5FCF0A4AC105D211 CRC64;

Query Match 42.1%; Score 24; DB 4; Length 22;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 PKAPTE 11
 DB 1 PEAPNE 6

RESULT 13
 ID 09PSB6 PRELIMINARY; PRT; 25 AA.
 AC 09PSB6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE TYROSINE KINASE (FRAGMENT).
 GN Xenopus laevis (African clawed frog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OX Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95280092; PubMed=7772253;
 RA Islam N., Guimond A., Sanchez A., Moss T.;
 RT "An analysis of Xenopus tyrosine kinase genes and their expression in
 RT early development."
 RL DNA Cell Biol. 13:719-729(1994).
 DR INTERPRO: IPR000719; -
 DR PRAM: PR000669; pkinase.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR SEQUENCE 25 AA; 2898 MW; 8DB74A313AEDC4C CRC64;

Query Match 42.1%; Score 24; DB 13; Length 25;
 Best Local Similarity 71.4%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 TAPKAPT 10
 DB 4 TAPEAMT 10

RESULT 14
 ID 09RLM9 PRELIMINARY; PRT; 27 AA.
 AC 09RLM9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PORA PROTEIN (FRAGMENT).
 GN PORA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-19/92;
 RA Wedge E., Gaugant D.A., Musacchio A., Saunders N.B., Zollinger W.D.;
 RT "Redesignation of a purported P1.15 subtype-specific meningococcal
 RT monoclonal antibody as a P1.19-specific reagent.";
 RL Clin. Diagn. Lab. Immunol. 6:639-642(1999).
 DR EMBL: AJ012728; CAA10151.1; -;
 FT NON_TER 1
 FT NON_TER 27
 SO SEQUENCE 27 AA; 2839 MW; 4DAF1FC85855E5FC CRC64;

Query Match 42.1%; Score 24; DB 2; Length 27;
 Best Local Similarity 55.6%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 QOTAPKAPT 10
 DB 12 QOTPOSQPT 20

RESULT 15

ID Q910I1 PRELIMINARY; PRT: 29 AA.
 AC Q910I1;
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
 DE TAT PROTEIN (FRAGMENT).
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT 17;
 RA Yamada T., Iwamoto A.;
 RT "Comparison of proviral accessory genes between long-term
 RT nonprogressors and progressors of human immunodeficiency virus type 1
 RT infection.";
 RL Arch. Virol. 145:1021-1027(2000).
 DR EMBL: AB034453; BAA93910.1; -;
 FT NON_TER 1
 SO SEQUENCE 29 AA; 3013 MW; 83CCFF3D51DA7255 CRC64;

Query Match 42.1%; Score 24; DB 12; Length 29;
 Best Local Similarity 45.5%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QOCTAPKAPTE 11
 DB 4 OPRGDPGPT 14

Search completed: February 13, 2001, 13:06:29
 Job time: 311 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:02:02 ; Search time 44.34 Seconds
(without alignments)
9.254 Million cell updates/sec

Title: us-09-372-036-30

Perfect score: 60

Sequence: 1 STPVAPRQEVKK 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 151408

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT:*

9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT:*

10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	12	14	R45172
2	60	100.0	21	16	R73891
3	51	85.0	10	14	R45173
4	41	68.3	9	14	R45168
5	36	60.0	7	16	R73903
6	32.5	54.2	11	14	R54624
7	32	53.3	6	14	R54615
8	32	53.3	15	11	R17929
9	32	53.3	15	14	R34337
10	32	53.3	20	14	R45159
11	32	53.3	27	20	W78130
12	31	51.7	30	21	Y69503

13	29	48.3	22	13	R28278
14	29	48.3	26	15	R62763
15	29	48.3	29	7	P61306
16	28	46.7	7	19	R21365
17	28	46.7	10	18	W42709
18	28	46.7	11	16	R75105
19	28	46.7	11	17	W10057
20	28	46.7	16	15	R58353
21	28	46.7	18	20	Y41105
22	28	46.7	21	16	R73894
23	28	46.7	27	17	W01470
24	28	46.7	28	20	Y03800
25	27	45.0	9	16	R79676
26	27	45.0	9	17	W07056
27	27	45.0	9	19	W70120
28	27	45.0	9	21	Y57975
29	27	45.0	11	16	W70126
30	27	45.0	15	16	R79629
31	27	45.0	16	19	W60628
32	27	45.0	16	19	W60629
33	27	45.0	16	19	W60630
34	27	45.0	16	19	W60634
35	27	45.0	20	15	R46816
36	27	45.0	25	16	R79982
37	27	45.0	27	11	R05105
38	27	45.0	28	15	R49685
39	26	43.3	15	19	W75624
40	26	43.3	15	19	W75625
41	26	43.3	15	17	W46779
42	26	43.3	19	17	R95686
43	26	43.3	20	20	W82295
44	26	43.3	23	20	W82310
45	26	43.3	27	9	P81791

ALIGNMENTS

RESULT 1

R45172 standard; Protein: 12 AA.

AC R45172:

DT 16-JUN-1994 (first entry)

DE Listeria p60 peptide epitope.

KW Listeria monocytogenes; antibodies; immunoassay; conjugate.

OS Synthetic.

PN DE4318450-A.

PD 16-DEC-1993.

PE 03-JUN-1993; 93DE-4318450.

PR 11-JUN-1992; 92DE-4219111.

PS 25-NOV-1992; 92DE-4239567.

PA (MERE) MERCK PATENT GMBH.

PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;

PI Hofmann G, Hubert A, Goebel W, Koehler S;

DR WPI; 1993-406956/51.

PT New primers for PCR detection of Listeria - including individual

PT species, also new peptide(s) for raising antibodies for

PT immunochemical detection

PS Disclosure; Fig 2; 19pp; German.

XX The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.

XX Sequence 12 AA:

Query Match 100.0%; Score 60; DB 14; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00048; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
 |||||
 Db 1 stpvaptevkk 12

RESULT 2

R73891 R73891 standard; peptide; 21 AA.

XX R73891;

XX 05-DEC-1995 (first entry)

XX *Listeria* monocytogenes protein p60 precursor peptide 144-164.

XX *Listeria* monocytogenes; protein p60 precursor; vaccine;

XX meningitis related homologous antigenic sequence; MRHAS; RV-1;

XX immunoassay; diagnosis; treatment; prophylactic; bacterial;

XX viral; peptide 144-164.

XX *Listeria* monocytogenes.

XX WO9509232-A.

XX 06-APR-1995.

XX 28-SEP-1994; 94WO-CN00516.

XX 28-SEP-1993; 93US-0127499.

XX (SHAR/) SHARMA L R.

XX (VALS/) VAN ALSTYNE D.

XX Sharma LR, Van Alstyne D;

XX WPI; 1995-147431/19.

XX New peptide(s) and corresp. antibodies for the treatment of

XX meningitis - the peptide(s) corresp. to homologous antigenic

XX sites on bacterial and viral agents and on chemokine(s), used for

XX detecting and preventing meningitis.

XX Claim 34; Page 74; 98pp; English.

XX R73913 is the *Listeria* monocytogenes protein p60 precursor. It

XX contains the meningitis related antigenic sequences (MRHAS) claimed

XX in R73891-R73894 and R73903-R73906, which are recognized by a

XX monoclonal antibody from the hybridoma Rubella virus (RV)-1. The

XX claimed MRHAS peptides may be used in immunoassays to diagnose the

XX presence of bacterial and/or viral meningitis agents in a sample,

XX or in prophylactic and therapeutic meningitis treatments. The

XX peptides may also be used as vaccines against meningitis.

XX Sequence 21 AA:

Query Match 100.0%; Score 60; DB 16; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.00086; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
 |||||
 Db 3 stpvaptevkk 14

RESULT 3

R45173 R45173 standard; Protein; 10 AA.

XX R45173;

XX 16-JUN-1994 (first entry)

XX *Listeria* p60 peptide epitope.

XX *Listeria* monocytogenes; antibodies; immunoassay; conjugate.

XX Synthetic.

XX DE4318450-A.

XX 16-DEC-1993.

XX 03-JUN-1993; 93DE-4318450.

XX 11-JUN-1992; 92DE-421911.

XX 25-NOV-1992; 92DE-4239567.

XX (MERE) MERCK PATENT GMBH.

XX Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;

XX Hofmann G, Bubert A, Goebel W, Koehler S;

XX WPI; 1993-406956/51.

XX New primers for PCR detection of *Listeria* - including individual

XX species, also new peptide(s) for raising antibodies for

XX immunochemical detection

XX Disclosure; Fig 2; 19pp; German.

XX The sequence is that of a *Listeria* p60 peptide epitope which

XX which may be used in the prodn. of antibodies for the detection

XX of *Listeria* by immunoassay (partic. ELISA). It may be used as

XX part of a method that allows determination of individual *Listeria*

XX species, esp. *L. monocytogenes*.

XX Sequence 10 AA:

Query Match 85.0%; Score 51; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVAPTOEVKK 12
 |||||
 Db 1 pvaptevkk 10

RESULT 4

R45168 R45168 standard; Protein; 9 AA.

XX R45168;

XX 16-JUN-1994 (first entry)

XX *Listeria* p60 peptide epitope.

XX *Listeria* monocytogenes; antibodies; immunoassay; conjugate.

XX Synthetic.

XX DE4318450-A.
 PN
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PS
 XX
 PS Disclosure; Fig 2; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 SQ Sequence 9 AA:
 Query Match 68.3%; Score 41; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2,1e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 STRPVAPRQ 8
 |||||
 DB 2 strpvaprq 9
 RESULT 5
 R73903
 ID R73903 standard; peptide; 7 AA.
 XX
 AC R73903;
 XX
 DT 05-DEC-1995 (first entry)
 XX
 DE Listeria monocytogenes protein P60 precursor peptide 151-157.
 XX
 KM Listeria monocytogenes; protein P60 precursor; vaccine;
 KM meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KM immunoassay; diagnosis; treatment; prophylactic; bacterial;
 XX viral; peptide 151-157.
 XX
 OS Listeria monocytogenes.
 XX
 PN WO9509232-A.
 PD 06-APR-1995.
 XX
 PF 28-SEP-1994; 94WO-CA00516.
 XX
 PR 28-SEP-1993; 93US-0127499.
 XX
 PA (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX
 PI Sharma LR, Van Alstyne D;
 DR WPI; 1995-147431/19.
 XX

PT New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 PS Claim 35; Page 76; 98pp; English.
 XX
 CC R73913 is the Listeria monocytogenes protein P60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in R73891-R73894 and R73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 CC
 SQ Sequence 7 AA:
 Query Match 60.0%; Score 36; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2,1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 PQGEVKK 12
 |||||
 DB 1 ptegvkk 7
 RESULT 6
 R54624
 ID R54624 standard; Protein; 11 AA.
 XX
 AC R54624;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria innocua p60 peptide epitope.
 XX
 KM Antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 OS
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PS
 XX
 PS Disclosure; Fig 5; 19pp; German.
 XX
 CC The sequence is that of a Listeria innocua p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species.
 CC
 SQ Sequence 11 AA:

Query Match 54.2%; Score 32.5; DB 14; Length 11;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 STVPAPTOEVKK 12
 ||||| |||||
 DB 1 scpvv-kgevvk 11

RESULT 7
 R54615
 ID R54615 standard; protein: 6 AA.
 AC R54615;
 XX
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria p60 peptide epitope.
 XX
 KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 PN DE4318450-A.
 XX
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 XX
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERCK) MERCK PATENT GMBH.
 XX
 PI Schuber P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 DR WPI: 1993-406956/51.
 XX
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PS Disclosure; Page 3; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 SQ Sequence 6 AA;

Query Match 53.3%; Score 32; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PVAPAQ 8
 |||||
 DB 1 pvapq 6

RESULT 8
 Y17929
 ID Y17929 standard; peptide: 15 AA.
 AC Y17929;
 XX
 XX
 DT 30-JUL-1999 (first entry)
 XX
 DE Synthetic peptide derived from HTLV envelope sugar protein.
 XX

KW Hydrophilic peptide; antigen determinant; envelope sugar protein;
 KW HTLV-I; HTLV-II; B lymphatic corpuscle; gp46; gp63; tetanus toxoid.
 OS Synthetic.
 OS Human lymphotropic virus type 1.
 XX
 PN JP02209889-A.
 XX
 PD 21-AUG-1990.
 XX
 PF 08-FEB-1989; 89JP-0029551.
 XX
 PR 30-JAN-1989; 89US-0303436.
 XX
 PR 08-FEB-1988; 88US-0153420.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 DR WPI: 1990-344000/46.
 XX
 XX
 PT Synthetic hydrophilic peptide - comprises 25 unit aminoacid that
 PT corresponds to at least one antigen determinant of envelope sugar
 PT protein(s) of HTLV-I and HTLV-II
 XX
 PS Claim 5; Page 1; 15pp; Japanese.
 XX
 CC The invention relates to new synthetic hydrophilic peptides (Y17922-934)
 CC that correspond to at least one of antigen determinants of envelope sugar
 CC proteins of HTLV-I and HTLV-II identified in the B lymphatic corpuscle.
 CC When bonded covalently to a carrier molecule, the peptides can induce the
 CC production of an antibody having a high titre to the gp46 and gp63
 CC envelope sugar proteins of HTLV-I and HTLV-II in mammals. The carrier
 CC molecule is preferably a tetanus toxoid and selected from the group of
 CC sequences shown in Y17935-39. The carrier molecule is preferably bonded
 CC to the peptide through at least one spacer molecule (preferably a
 CC dipeptide glycine-glycine). The peptides form effectively immunological
 CC response to factors causing virus HTLV-I and HTLV-II. The method also
 CC provides an effective conjugate having the peptide.
 CC
 SQ Sequence 15 AA;

Query Match 53.3%; Score 32; DB 11; Length 15;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 STVPAPTOEV 10
 |||||
 DB 5 sspscptqpv 14

RESULT 9
 R34237
 ID R34237 standard; peptide: 15 AA.
 AC R34237;
 XX
 DT 04-AUG-1993 (first entry)
 XX
 DE HTLV-II envelope glycoprotein fragment 1.
 XX
 KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies.
 XX
 OS Synthetic.
 PN WO9306843-A.
 XX
 PD 15-APR-1993.
 XX
 PF 08-OCT-1992; 92WO-US08405.
 XX
 PR 08-OCT-1991; 91US-0771553.
 XX

PA (UYDU-) UNIV DUKE.
 XX
 PI Haynes BF, Palker TJ;
 XX
 DR WPI; 1993-134125/16.
 XX
 PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein -
 PT useful for detecting anti-HTLV-I and -II antibodies and as
 PT vaccine against HTLV
 XX
 PS Claim 5; Page 13; 50pp; English.
 CC The sequence of peptide 1 corresponds to residues 30-44 from the
 CC HTLV-II envelope glycoprotein. When covalently linked
 CC to a carrier mol. the hydrophilic peptide can induce in a mammal the
 CC prodn. of high titres of antibodies to gp46 envelope glycoprotein from
 CC HTLV-I or -II. The peptide and carrier may be used in vaccines against
 CC HTLV-I or -II infection. The peptide may be used in a diagnostic
 CC assay to detect the presence and titre of anti-HTLV antibodies.
 CC See also R34225-57.
 CC
 XX
 SO Sequence 15 AA;
 Query Match 53.3%; Score 32; DB 14; Length 15;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STPVAPTOEV 10
 DB 5 sspscptcpv 14
 RESULT 10
 R45159
 ID R45159 standard; Protein; 20 AA.
 XX
 AC R45159;
 XX
 DT 16-JUN-1994 (first entry)
 XX
 DE Listeria p60 peptide epitope.
 XX
 KW Listeria monocytogenes; antibodies; immunoassay; conjugate.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 1..7
 FT Region /note= "opt. 0-7 amino acid residues"
 FT 14..20
 FT Region /note= "opt. 0-7 amino acid residues"
 XX
 DE4318450-A.
 PN 16-DEC-1993.
 PD
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Linxweiler W, Burger C;
 PI Hofmann G, Buber A, Goebel W, Koehler S;
 XX
 DR WPI; 1993-406956/51.
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX

PS Claim 3; Page 4; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 XX
 SO Sequence 20 AA;
 Query Match 53.3%; Score 32; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PVAPTO 8
 DB 8 pvaptq 13
 RESULT 11
 W78130
 ID W78130 standard; Protein; 27 AA.
 XX
 AC W78130;
 XX
 DT 13-APR-1999 (first entry)
 XX
 DE Human secreted protein encoded by gene 5 clone HPBD36.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 27
 FT /label= unknown
 XX
 PN W09856804-A1.
 PD
 PD 17-DEC-1998.
 XX
 PE 11-JUN-1998; 98MO-US12125.
 XX
 PR 02-OCT-1997; 97US-0061060.
 PR 13-JUN-1997; 97US-0049547.
 PR 13-JUN-1997; 97US-0049548.
 PR 13-JUN-1997; 97US-0049549.
 PR 13-JUN-1997; 97US-0049550.
 PR 13-JUN-1997; 97US-0049550.
 PR 13-JUN-1997; 97US-0049606.
 PR 13-JUN-1997; 97US-0049607.
 PR 13-JUN-1997; 97US-0049608.
 PR 13-JUN-1997; 97US-0049609.
 PR 13-JUN-1997; 97US-0049610.
 PR 13-JUN-1997; 97US-0049611.
 PR 13-JUN-1997; 97US-0050566.
 PR 13-JUN-1997; 97US-0050901.
 PR 13-JUN-1997; 97US-0052889.
 PR 08-JUL-1997; 97US-0051919.
 PR 18-AUG-1997; 97US-0055984.
 PR 12-SEP-1997; 97US-0058665.
 PR 12-SEP-1997; 97US-0058668.
 PR 12-SEP-1997; 97US-0058669.
 PR 12-SEP-1997; 97US-0058750.
 PR 12-SEP-1997; 97US-0058971.
 PR 12-SEP-1997; 97US-0058972.

PR 12-SEP-1997; 97US-0058875.
 PR 02-OCT-1997; 97US-0060834.
 PR 02-OCT-1997; 97US-0060841.
 PR 02-OCT-1997; 97US-0060844.
 PR 02-OCT-1997; 97US-0060865.
 PR 02-OCT-1997; 97US-0061059.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Brewer LA, Ederer R, Ferlie AM, Feng P, Greene JM, Lafleur DW;
 PI Moore PA, NJ J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
 PI Yu GL;
 XX WPI: 1999-080881/07.
 DR N-PSDB; X04315.
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 11: Page 266; 380pp; English.
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. X04302) for increasing the stability of the fused protein
 CC as compared to the human protein only.
 CC The invention relates to 86 novel genes and their fragments (nucleic acid
 CC sequences: X04311-X04410; amino acid sequences W78126-W78225) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 86 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X04311 for described
 CC uses).
 XX
 SQ Sequence 27 AA:
 QY 3 PVAPTOEVKK 12
 DB 9 pvaqtetsqk 18
 QY 3 PVAPTOEVKK 12
 DB 9 pvaqtetsqk 18
 RESULT 12
 ID Y69503
 XX Y69503 standard; peptide: 30 AA.
 AC Y69503;
 XX
 DT 10-APR-2000 (first entry)
 DE C-terminus of MMLV ecotropic env variant construct 2.
 XX
 XX Envelope protein; env; gp70; ecotropic; MMLV; mCAT1 receptor;
 KM targeted delivery; gene therapy vehicle; retroviral; phage display;
 KM mutant; muteln.
 XX
 XX Moloney murine leukemia virus.
 OS Synthetic.
 XX
 PN EP972841-A1.
 XX
 PD 19-JAN-2000.
 XX
 PF 20-MAY-1999; 99EP-0201592.
 XX
 PK 20-MAY-1998; 98EP-0201678.

XX (INTR-) INTRIGENE BV.
 PA Van Es H;
 PI
 XX WPI: 2000-099858/09.
 DR
 XX
 PT New methods for producing gene transfer vehicles, useful for targeted
 PT delivery of substances to cells -
 XX
 PS Example 1; Page 17; 31pp; English.
 CC This sequence represents the C-terminal sequence of a Moloney
 CC murine leukaemia virus (MMLV) gp70 envelope (env) protein mutant,
 CC construct 2, used in an exemplification of the present invention.
 CC The gp70 protein is one of two components of retroviral env proteins,
 CC and is derived from the env gene-encoded precursor via proteolytic
 CC cleavage. gp70 is responsible for binding a host cell-surface receptor,
 CC thereby determining host range of the virus. MMLV is an ecotropic virus,
 CC which binds to target cells via their mCAT1 cationic amino acid
 CC transporter. The invention relates to a method for selecting at least one
 CC mutant viral protein (e.g., gp70) as a ligand capable of binding to a
 CC cell-surface receptor. This method comprises displaying one or more
 CC mutant viral proteins on the surface of a microorganism (e.g., a
 CC filamentous phage) and selecting the microorganism for its ability to
 CC bind to the cell-surface receptor. The invention also encompasses a
 CC method for selecting for a filamentous phage expressing a protein capable
 CC of binding to a ligand. The methods of the invention are used to select a
 CC protein, or a filamentous phage displaying that protein, which is capable
 CC of binding to a cell surface receptor. These methods may be used to
 CC produce a virus-like particle or gene delivery vehicle which can be used
 CC for gene transfer. This is useful for the targeted delivery of
 CC substances to cells, such as nucleotides for use in gene therapy, or
 CC compounds that kill tumour cells. The methods can be used to block the
 CC productive infection of cells in a human patient, and mutant envelope
 CC displaying phages that block a receptor can be used to treat pathogenic
 CC virus infections. The methods are therefore especially useful for human
 CC medicine. The gene transfer vehicles produced using the methods of the
 CC invention enable better application of gene transfer therapy than prior
 CC art methods. The prior art use of retroviruses are not highly effective
 CC because all known env variants have a broad infection spectrum in
 CC common. The new methods modify the infection spectrum of virus-like
 CC particles, producing increased specificity and efficiency.
 XX
 SQ Sequence 30 AA:
 QY 2 TPVAPTO 8
 DB 4 tpisptq 10
 QY 2 TPVAPTO 8
 DB 4 tpisptq 10
 RESULT 13
 ID R28278
 XX R28278 standard; Protein: 22 AA.
 AC R28278;
 XX
 DT 31-MAR-1993 (first entry)
 DE Sequence of coxsacke mosaic virus (CPMV) coat protein VP23 coding
 DE sequence after site-directed mutagenesis.
 XX
 XX Coat protein; VP23; M RNA; CPMV; ss.
 OS Synthetic.
 XX
 PN WO9218618-A.
 XX

PD 29-OCT-1992.
 XX
 PF 02-APR-1992; 92WO-GB00589.
 XX
 PR 19-APR-1991; 91GB-0008386.
 XX
 PA (AGRI-) AGRIC GENETICS CO.
 PA (PURD) PURDUE RES FOUND.
 XX
 PI Johnson JE, Lomonosoff GP;
 XX
 DR WPI: 1992-382105/46.
 DR P-PSDB: R28278.
 XX
 PT Modified plant viruses contg. foreign antigenic peptide - for
 PT prodn. of vaccines against viruses e.g. foot and mouth, HIV,
 PT hepatitis-A, etc.
 XX
 PS Example; Fig 8: 51pp; English.
 PS
 XX Both PFMDV amd its derivative PMT7-FMDV-1 have a straightforward
 CC insertion into the beta-B-beta-C loop of VP23. To limit the increase
 CC in size of the loop upon insertion of a foreign sequence, a replacement
 CC vector was designed where the foreign sequence would replace the ntural
 CC beta-B-beta-C loop in VP23 rather than be added to it. In the
 CC nucleotide sequence of the region of the CPV genome encoding VP23 a
 CC single silent base change (U to C) at posn. 2740 creates a unique AatII
 CC site at amino acid valine 27. The creation of the AatII site enables
 CC the nucleotide sequence encoding the six amino acids from the native
 CC beta-B-beta-C loop in CPV to be removed by digestion with NheI and
 CC AatII. The sequence can then be replaced by any sequence with NheI-
 CC and AatII-compatible ends.
 CC
 XX Sequence 22 AA;
 SQ

Query Match 48.3%; Score 29; DB 13; Length 22;
 Best Local Similarity 60.0%; Pred. NO. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 STPVAPTOEV 10
 :|||:|:|
 Db 5 stpapsfadv 14

RESULT 14
 R62763
 ID R62763 standard; Protein; 26 AA.
 XX
 AC R62763;
 XX
 DT 07-JUN-1995 (first entry)
 DE Synthetic peptide E.
 XX
 KM Stabilisation; toxic; peroxisome; yeast; food additive; brazil nut.
 XX
 OS Synthetic.
 XX
 PN WO9424289-A.
 XX
 PD 27-OCT-1994.
 XX
 PF 19-APR-1994; 94WO-FR00438.
 XX
 PR 19-APR-1993; 93FR-0004583.
 XX
 PA (EURO-) EUROLYSINE.
 XX
 PI Ito H, Labat N, Niclaud J, Pardo D, Raynal A, Sugimoto S;
 XX
 DR WPI: 1994-341868/42.
 DR N-PSDB: Q73070.
 DR

XX
 PT Improving stability of protein or peptide in yeast - by
 PT expressing with a peroxisomal targeting sequence, allowing
 PT accumulation of unstable or toxic products, and new yeast strains
 PT useful as food additives
 XX
 PS Claim 9; Figure 2; 40pp; French.
 PS
 XX Stabilisation of a non-peroxisomal protein or peptide that is
 CC unstable in, or toxic for, a yeast and made by expressing a
 CC heterologous DNA sequence in the yeast, comprises expressing it with
 CC a sequence that targets that targets to stabilise/detoxify in the
 CC yeast peroxisomes. The method is especially used when the non-
 CC peroxisomal protein is the 2S storage protein (See R62762) of Brazil
 CC nuts or the synthetic peptides E (this sequence) and ELE (See
 CC R62764). Yeast expressing these proteins are useful as food
 CC additives (having a high content of essential amino acids).
 CC
 XX Sequence 26 AA;
 SQ

Query Match 48.3%; Score 29; DB 15; Length 26;
 Best Local Similarity 36.4%; Pred. NO. 1.4e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 STPVAPTOEVK 11
 :||:|:|:|
 Db 15 atpispangak 25

RESULT 15
 P61306
 ID P61306 standard; Protein; 29 AA.
 XX
 AC P61306;
 XX
 DT 05-JUN-1991 (first entry)
 DE Trans-acting transcription factor of the HTLV-III ARV genome exon 2.
 XX
 KM Viral surface glycoprotein; vaccine.
 XX
 OS Human t-cell lymphotropic virus.
 XX
 PN WO8505636-A.
 XX
 PD 19-DEC-1985.
 XX
 PF 24-MAY-1985; 85WO-US00985.
 XX
 PR 25-MAY-1984; 84US-0614297.
 PR 06-DEC-1985; 85US-0806263.
 XX
 PA (DANA-) DANA-FARBER CANCER.
 XX
 PI Haseltine WA, Sodroski JG, Rosen CA;
 XX
 DR WPI: 1986-006897/01.
 DR N-PSDB: N60931.
 XX
 PT System for increasing gene expression in host cells - comprises
 PT vector including cis-acting element and trans acting segment of
 PT retro-virus DNA.
 XX
 PS Disclosure; Fig 5; 67pp; English.
 PS
 XX Placing the trans-acting sequence in a cell with an expression
 CC vector carrying the gene to be expressed and a cis-acting element,
 CC allows for the increased yield of the product. The system is
 CC especially useful in the isolation of viral surface proteins as
 CC antigens or vaccines.
 CC
 XX Sequence 29 AA;
 SQ

Query Match 48.3%; Score 29; DB 7; Length 29;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 PVAPRQEVKK 12
| | | | |
| | | | |
Db 9 ptgpteskkk 18

Search completed: February 13, 2001, 13:02:02
Job Time: 83 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:03:17 ; Search time 32.52 Seconds
(without alignments)
6.626 Million cell updates/sec

Title: US-09-372-036-30
Perfect score: 60
Sequence: 1 STPAVPTGEVKK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 111283

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	12	2	US-08-456-670B-30
2	60	100.0	21	1	US-08-127-499A-27
3	60	100.0	21	1	US-08-482-847-27
4	51	85.0	10	2	US-08-456-670B-31
5	41	68.3	9	2	US-08-456-670B-26
6	36	60.0	7	1	US-08-127-499A-28
7	36	60.0	7	1	US-08-482-847-28
8	35	58.3	12	3	US-08-389-011-16
9	35	58.3	12	3	US-08-403-917A-16
10	35	58.3	12	3	US-08-389-011-7
11	35	58.3	26	2	US-08-403-917A-7
12	32.5	54.2	11	2	US-08-456-670B-35
13	32	53.3	12	2	US-08-389-011-17
14	32	53.3	12	2	US-08-389-011-18
15	32	53.3	12	3	US-08-403-917A-17
16	32	53.3	12	3	US-08-403-917A-18
17	32	53.3	15	1	US-08-116-733-15
18	32	53.3	20	2	US-08-456-670B-17
19	30	50.0	12	2	US-08-389-011-15
20	30	50.0	12	3	US-08-403-917A-15
21	30	50.0	17	1	US-08-553-703A-7
22	30	50.0	17	2	US-09-006-021-7
23	29	48.3	23	2	US-08-471-048-13
24	29	48.3	23	2	US-08-471-048-15
25	29	48.3	23	2	US-08-612-858-12
26	29	48.3	23	2	US-08-612-858-14
27	29	48.3	23	3	US-08-137-032-13
28	29	48.3	23	3	US-08-137-032-15

29	28	46.7	11	5	5200183-12	Patent No. 5200183
30	28	46.7	16	1	US-08-307-724B-35	Sequence 35, Appl
31	28	46.7	21	1	US-08-127-499A-33	Sequence 33, Appl
32	28	46.7	21	1	US-08-482-847-33	Sequence 33, Appl
33	28	46.7	28	2	US-08-942-423-9	Sequence 9, Appl
34	27	45.0	9	1	US-08-178-570-29	Sequence 29, Appl
35	27	45.0	9	2	US-08-340-283-81	Sequence 81, Appl
36	27	45.0	9	3	US-08-369-643-29	Sequence 29, Appl
37	27	45.0	9	4	PCT-US95-00147-29	Sequence 29, Appl
38	27	45.0	12	2	US-08-354-685-2	Sequence 2, Appl
39	27	45.0	12	2	US-08-389-011-13	Sequence 13, Appl
40	27	45.0	12	2	US-08-389-011-14	Sequence 14, Appl
41	27	45.0	12	2	US-08-389-011-19	Sequence 19, Appl
42	27	45.0	12	3	US-08-403-917A-13	Sequence 13, Appl
43	27	45.0	12	3	US-08-403-917A-14	Sequence 14, Appl
44	27	45.0	12	3	US-08-403-917A-19	Sequence 19, Appl
45	27	45.0	15	2	US-08-687-956A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-456-670B-30
Sequence 30, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWELLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
SPRAIN: EGD
US-08-456-670B-30

Query Match 100.0%; Score 60; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
DB 1 STPVAPTOEVKK 12

RESULT 2
US-08-127-499A-27
Sequence 27, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-27

Query Match 100.0%; Score 60; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
DB 3 STPVAPTOEVKK 14

RESULT 3
US-08-482-847-27
Sequence 27, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-27

Query Match 100.0%; Score 60; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVAPTOEVKK 12
DB 3 STPVAPTOEVKK 14

RESULT 4
US-08-456-670B-31
Sequence 31, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
LISTERIAS

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

Query Match 85.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PVAPTOEVKK 12
| | | | | | | | | |
DB 1 PVAPTOEVKK 10

RESULT 5
US-08-456-670B-26
Sequence 26, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAWELZIK, MARTINA
APPLICANT: LINXWETLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-26

Query Match 68.3%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STPVAPRO 8
| | | | | | | |
DB 2 STPVAPRO 9

RESULT 6
US-08-127-499A-28
Sequence 28, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-28

Query Match 60.0%; Score 36; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PROEVKK 12
111111
DB 1 PROEVKK 7

RESULT 7
US-08-482-847-28
Sequence 28, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-28

Query Match 60.0%; Score 36; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PROEVKK 12
111111
DB 1 PROEVKK 7

RESULT 8
US-08-389-011-16
Sequence 16, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
TITLE OF INVENTION: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TWO, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,003-1-COM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 12
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-16

Query Match 58.3%; Score 35; DB 2; Length 12;
Best Local Similarity 58.3%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
| | | | | | | | | | | | | |
Db 1 SLPTPTREPKK 12

RESULT 9
US-08-403-917A-16
Sequence 16, Application US/08403917A
Patent No. 6010913

GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANMECHELEN, EUGEN;

APPLICANT: VAN DE VOORDE, ANDRE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE

TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/256,167

FILING DATE: 27-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/244,951

FILING DATE: 13-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/03499

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/92/403403.6

FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410,003-1

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 12

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

US-08-403-917A-16

Query Match 58.3%; Score 35; DB 3; Length 12;
Best Local Similarity 58.3%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
| | | | | | | | | | | | | |
Db 1 SLPTPTREPKK 12

RESULT 10
US-08-389-011-7
Sequence 7, Application US/08389011
Patent No. 5861257

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE

TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/389,011

FILING DATE: 15-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,916

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/244,951

FILING DATE: 13-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/03499

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/92/403403.6

FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410,003-1-CON

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 26

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

US-08-389-011-7

Query Match 58.3%; Score 35; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 STPVAPTOEVK 12
1 1 1 1 1 1
DB 9 SLTPPTREPK 20

RESULT 11

US-08-403-917A-7
Sequence 7, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGENE;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-7

Query Match 58.3%; Score 35; DB 3; Length 26;
Best Local Similarity 58.3%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 STPVAPTOEVK 12
1 1 1 1 1 1
DB 9 SLTPPTREPK 20

RESULT 12
US-08-456-670B-35

Sequence 35, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELIZ, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BOBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STERAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELAND & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria innocua
US-08-456-670B-35

Query Match 54.2%; Score 32.5; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 STPVAPTOEVK 12
1 1 1 1 1 1
DB 1 STPVV-KOEVK 11

RESULT 13
US-08-389-011-17

Sequence 17, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-17

Query Match 53.3%; Score 32; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PVAPTOEVKK 12
1 11:111
2 PTPPTREPKK 11

Db

RESULT 14
US-08-389-011-18
Sequence 18, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

APPLICANT: VANDERMEEREN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-18

Query Match 53.3%; Score 32; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PVAPTOEVKK 12
1 11:111
Db 1 PTPPTREPKK 10

Db

RESULT 15
US-08-403-917A-17
Sequence 17, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDERMEEREN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: PROTEIN TAU HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIEMAN & MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,917A
 FILING DATE: 19-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/256,167
 FILING DATE: 27-JUN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/244,951
 FILING DATE: 13-JUN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP/92/403403.6
 FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MUSERLIAN
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 410,003-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-8002
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown

Query Match	53.3%	Score 32	DB 3	Length 12
Best Local Similarity	60.0%	Pred. No. 6.4		
Matches	6	Conservative	1	Mismatches 3
				Indels 0
				Gaps 0
Qy	3	PVAPVQEVKK	12	
	1	11:111		
db	2	PTPTTREPCK	11	

Search completed: February 13, 2001, 13:03:17
Job time: 157 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:02:41 : Search time 35.7 seconds
(without alignments)
22.824 Million cell updates/sec

Title: US-09-372-036-30
Perfect score: 60
Sequence: 1 STPVAPTOEVKK 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 6242

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	48.3	12	2 JU0356	cyctoleonurinin -
2	29	48.3	15	2 S68731	bleomycin-binding
3	26	43.3	24	2 IS0387	c-myc protein - ch
4	26	43.3	27	2 S55234	flavodoxin isoform
5	25	41.7	18	2 A28027	protein P2 - curle
6	25	41.7	20	2 B56385	nitrophenol 2 - Rh
7	25	41.7	27	2 A49236	fibroblast-activat
8	24	40.0	18	2 A61220	epsilon receptor m
9	24	40.0	20	2 A37111	ribulose-bisphosph
10	24	40.0	21	2 S32883	DNA gyrase chain A
11	24	40.0	21	2 PH1231	chlorogenic acid o
12	24	40.0	24	2 A61505	pollen allergen ph
13	24	40.0	27	2 F39690	neural cell adhesi
14	23	38.3	14	2 A60158	disaggregatase - M
15	23	38.3	20	2 A61150	30K allergen - vel
16	23	38.3	20	2 S38291	seed protein ws-6
17	23	38.3	26	2 F61491	flavodoxin isoform
18	23	38.3	29	1 TNLJBR	trans-activating t
19	23	38.3	30	2 G71359	hypothetical prote
20	23	38.3	10	2 JP0072	ribosomal protein
21	22	36.7	16	2 PH1790	T cell receptor al
22	22	36.7	17	2 S50901	chlorophyll a/b-bi
23	22	36.7	20	2 S72501	protein kinase C 1
24	22	36.7	23	2 A49221	14K aggregative ad
25	22	36.7	24	2 A56753	lysine-rich 18K pr
26	22	36.7	24	2 PC2313	X-Pro aminopeptida
27	22	36.7	24	2 S23121	1H-3-hydroxy-4-oxo
28	22	36.7	25	2 I40692	cenA protein (19A1
29	22	36.7	25	2 I40692	

30	22	36.7	25	2 PC4389	sulfite reductase
31	22	36.7	27	2 S09504	homeotic protein c
32	22	36.7	30	2 S55462	mers protein homol
33	22	36.7	30	2 A33308	thrombomodulin - I
34	21	35.0	13	2 PC1149	equilatorin 1A - s
35	21	35.0	15	2 S21242	H+-transporting AT
36	21	35.0	16	2 A24099	crystal protein, 2
37	21	35.0	16	2 A42411	myosin light chain
38	21	35.0	19	2 A33361	CAMP-regulated pho
39	21	35.0	20	2 S38294	32K allergen - com
40	21	35.0	20	2 C56385	nitrophenol 3 - Rh
41	21	35.0	20	2 S15861	estrogen receptor
42	21	35.0	22	2 I46582	Ca2+ ATPase, adult
43	21	35.0	22	2 JC1488	hypothetical 2.5K
44	21	35.0	29	2 S03277	photosystem II 5K
45	21	35.0	30	2 B60291	30K serine protein

ALIGNMENTS

RESULT 1
JU0356
cyctoleonurinin - sagebrush motherwort
C:Species: leonurus artemisia (sagebrush motherwort)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JU0356
R:Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.
Chem. Pharm. Bull. 39, 712-715, 1991
A:Title: Cyctoleonurinin, a cyclic peptide from Leonuri fructus.
A:Reference number: JU0356; WUID:91300597
A:Accession: JU0356
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIN>

Query Match 48.3% Score 29; DB 2; Length 12;
Best Local Similarity 71.4% Pred. No. 29;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TPVAPTO 8
Db 2 TPACPTQ 8

RESULT 2
S68731
bleomycin-binding protein - Staphylococcus aureus (fragment)
C:Species: Staphylococcus aureus
C>Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C:Accession: S68731
R:Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Na
FEBS Lett. 362, 80-84, 1995
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing St
al characterization.
A:Reference number: S68730; WUID:95212588
A:Accession: S68731
A:Molecule type: protein
A:Residues: 1-15 <SUG>
A:Experimental source: strain B-26
C:Keywords: antibiotic resistance

Query Match 48.3% Score 29; DB 2; Length 15;
Best Local Similarity 41.7% Pred. No. 36;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 STPVAPTOEVKK 12
Db 4 STPALPVGDIDK 15

```

RESULT      3
150387
c-myc protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: 150387
R:Marway, D.; Payne, G.; Varmus, H.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 843-847, 1984
A:Title: Proviral deletions and oncogene base-substitutions in insertional mutagenized
A:Reference number: 150387; MUID:84144799
A:Accession: 150387
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <MES>
A:Cross-references: GB:K01440; NID:g212357; PIDN:AAA48964.1; PID:g212358

Query Match      43.3%; Score 26; DB 2; Length 24;
Best Local Similarity 40.0%; Pred. No. 2,1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY      3 PVAPTOEVK 12
      |||:::|
Db      2 PPAPSEDIMK 11

RESULT      4
555234
flavodoxin isoform I - Chlorella fusca
C:Species: Chlorella fusca
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C:Accession: S55234
R:Pelegato, M.L.; Ayora, S.; Inda, L.A.; Gomez-Moreno, C.
Biochem. J. 302, 807-811, 1994
A:Title: Isolation and characterization of two different flavodoxins from the eukaryote
A:Reference number: S55234; MUID:95031921
A:Accession: S55234
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-27 <PEL>

Query Match      43.3%; Score 26; DB 2; Length 27;
Best Local Similarity 60.0%; Pred. No. 2,4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      1 STPVAPTOEV 10
      |||||
Db      7 STATGKTQEV 16

RESULT      5
A28027
protein p2 - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C:Accession: A28027
R:Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid
A:Reference number: A94167
A:Accession: A28027
A:Molecule type: protein
A:Residues: 1-18 <BAU>
A:Note: 14-Arg was also found

Query Match      41.7%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2,4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      3 PVAPTOEV 10
      ||| |

```

```

Db      10 P1A6Q6NL 17

RESULT      6
B56385
nitrophenol 2 - Rhodnius prolixus (fragment)
N:Alternate names: nitric oxide-carry protein NP2
C:Species: Rhodnius prolixus
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C:Accession: B56385
R:Champagne, D.E.; Nussenzweig, R.H.; Ribeiro, J.M.C.
R: Biol. Chem. 270, 8691-8695, 1995
A:Title: Purification, partial characterization, and cloning of nitric oxide-carrying
A:Reference number: A56385; MUID:95238361
A:Accession: B56385
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <CHA>
C:Keywords: heme; salivary gland; vasodilator

Query Match      41.7%; Score 25; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY      1 STPVAPTOEVKK 12
      ||::||| | |
Db      3 STNISPKQGLDK 14

RESULT      7
A49236
fibroblast-activating factor - Porphyromonas gingivalis (fragment)
C:Species: Porphyromonas gingivalis
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A49236
R:Minhara, J.; Holt, S.C.
R: Infect. Immun. 61, 588-595, 1993
A:Title: Purification and characterization of fibroblast-activating factor isolated f
A:Reference number: A49236; MUID:93138782
A:Accession: A49236
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-27 <MIH>
A:Experimental source: W50
A:Note: sequence extracted from NCBI backbone (NCBIP:123245)

Query Match      41.7%; Score 25; DB 2; Length 27;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 STPVAPTOEV 10
      ||||| | |
Db      7 STPEAVTKTV 16

RESULT      8
A61220
epsilon receptor modulating protein (EC 3.4.21.-) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Mar-1996
C:Accession: A61220
R:Matsushita, S.; Katz, D.H.
R: Cell. Immunol. 137, 252-259, 1991
A:Title: The murine epsilon receptor modulating protein: a novel serine protease whic
A:Reference number: A61220; MUID:91356570
A:Accession: A61220
A:Molecule type: protein
A:Residues: 1-18 <MAT>
C:Comment: This serine proteinase from a T cell hybridoma does not reduce levels of C
C:Keywords: hydrolase; serine proteinase

```


disaggregatase - Methanosarcina mazel (strain LYC) (fragment)
C:Species: Methanosarcina mazel
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 07-May-1999
C:Accession: A60158
R:Xun, L.; Mah, R.A.; Boone, D.R.
Appl. Environ. Microbiol. 56, 3693-3698, 1990
A:title: Isolation and characterization of disaggregatase from Methanosarcina mazel LYC.
A:Reference number: A60158; MUID:91189693
A:Accession: A60158
A:Molecule type: protein
A:Residues: 1-14 <XUN>
C:Comment: Disaggregatase can release individual cells by hydrolyzing the characteristic

Query Match 38.3%; Score 23; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TPVAP 6
1111
DB 2 TPVAP 6

RESULT 15
A61150
2-oxoglutarate decarboxylase (EC 4.1.1.71) - Euglena gracilis (fragment)
C:Species: Euglena gracilis
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-Apr-1994
C:Accession: A61150
R:Shigeoka, S.; Nakano, Y
Arch. Biochem. Biophys. 288, 22-28, 1991
A:title: Characterization and molecular properties of 2-oxoglutarate decarboxylase from
A:Reference number: A61150; MUID:91378443
A:Accession: A61150
A:Molecule type: protein
A:Residues: 1-20 <SHI>
C:Keywords: carbon-carbon lyase; carboxy-lyase; homotetramer; mitochondrion

Query Match 38.3%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 APQEVK 11
11::11
DB 5 APVKDYK 11

Search completed: February 13, 2001, 13:02:42
Job time: 122 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:06:53 ; Search time 20.83 Seconds
(without alignments)
18,604 Million cell updates/sec

Title: US-09-372-036-30
Perfect score: 60
Sequence: 1 STPVAPTOEVKK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues
Total number of hits satisfying chosen parameters: 1785

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	25	41.7	17 1 JHBP_PLAVG	P56675 platypreria
2	24	40.0	21 1 GYRA_STRSH	P50071 streptomyc
3	23	38.3	27 1 IPPD_MOUSE	O60829 mus musculu
4	23	38.3	30 1 Y161_TREPA	O83196 treponema p
5	22	36.7	27 1 HM12_CAEEL	P17487 caenorhabdi
6	21	35.0	15 1 ATP2_SPIOL	P80083 spinnacia ol
7	21	35.0	15 1 UC08_MAIZE	P80614 zea mays (m
8	21	35.0	16 1 RL6_VIBPR	O56715 vibrio prot
9	21	35.0	19 1 CH10_CLOPA	P81338 clostridium
10	21	35.0	30 1 LAS1_PIG	P80171 sus scrofa
11	20	33.3	10 1 SPRC_RAHIT	P36233 oryctolagus
12	20	33.3	13 1 ODDA_CANPA	P49823 canis famli
13	20	33.3	19 1 RL10_CITFR	P43448 citrobacter
14	20	33.3	20 1 RL10_PROVU	P51411 proteus vul
15	20	33.3	22 1 RL10_KLEPN	P41190 klebsella
16	20	33.3	23 1 RL10_ENTCL	O47608 enterobacte
17	20	33.3	24 1 ALKB_SALTY	P37462 salmonella
18	20	33.3	24 1 DNAJ_STRAG	P55694 streptococc
19	20	33.3	29 1 RPS4_CLOKL	P38944 clostridium
20	19	31.7	9 1 DCML_PSECF	P19913 pseudomonas
21	19	31.7	13 1 UN02_PINPS	P16671 pinus pinas
22	19	31.7	20 1 APAL_ERYPA	P18647 erythrocebu
23	19	31.7	21 1 CH1C_PEA	P12133 plisum sativ
24	19	31.7	21 1 CXGT_CONTU	P17684 conus tulip
25	19	31.7	21 1 PSBF_STYNU	P12239 synechococc
26	19	31.7	22 1 ODPX_BOVIN	P22439 bos taurus
27	19	31.7	24 1 KPYK_CLOPA	P81344 clostridium
28	19	31.7	25 1 ACP_ALCPA	P80917 alcaligenes
29	19	31.7	25 1 RS20_THETH	P80382 thermus aqu
30	19	31.7	27 1 L52_ADE07	P05665 human adeno
31	19	31.7	29 1 HOXY_NOCOP	P22660 nocardiella op
32	19	31.7	29 1 IPRR_DESVH	P19371 desulfovibrio
33	19	31.7	30 1 TAT_HV12H	P12512 human immun

34	18	30.0	19 1 ITHA_PERAM	P19966 periplaneta.
35	18	30.0	19 1 TCBI_TRILIO	P80070 trichoderma
36	18	30.0	20 1 ACPH_BOVIN	P80227 bos taurus
37	18	30.0	21 1 MCT3_MOUSE	P21843 mus musculu
38	18	30.0	23 1 IBP2_PIG	P24853 sus scrofa
39	18	30.0	24 1 MDH_PLAVE	P19981 planomonosp
40	18	30.0	24 1 MDH_STRRS	P19983 streptocosp
41	18	30.0	25 1 DNAJ_MYCCA	P71500 mycoplasma
42	18	30.0	28 1 ORND_PLAOR	P25513 plachocella
43	18	30.0	29 1 PSAP_SYMP6	P31083 synechococc
44	18	30.0	29 1 TAT_HV123	P12510 human immun
45	17	28.3	12 1 TM2A_METWA	P80652 methanosarc

ALIGNMENTS

RESULT	ID	JHBP_PLAVG	STANDARD	PRT	17 AA.
1	JHBP_PLAVG				
AC	P56675:				
DT	15-JUL-1999 (Rel. 38, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	JUVENILE HORMONE-BINDING PROTEIN (FRAGMENT)				
GN	JHBP.				
OS	Platypreria virginialis (Ranchman's tiger moth).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;				
OC	Noctuidae; Arctidae; Platypreria.				
RN	[1]				
RP	SEQUENCE.				
RA	Prestwich G.D., Atkinson J.K.:				
RT	"Rapid purification and N-terminal amino acid sequence of a				
RT	photoaffinity-labeled juvenile hormone binding protein from an arctiid				
RT	moth larva, Platypreria virginialis."				
RL	Insect Biochem. 20:801-807(1990).				
CC	-1- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING HYDROLYZED BY				
CC	GENERAL ESTERASES BY COMBINING WITH IT SPECIFICALLY.				
CC	-1- SUBCELLULAR LOCATION: SECRETED.				
FT	NON_TER				
FT	SEQUENCE 17 AA: 1880 MM: B1205F09732DA8A CRC64;				
SO	SEQUENCE 17 AA: 1880 MM: B1205F09732DA8A CRC64;				
Query Match	41.7%: Score 25; DB 1; Length 17;				
Best local Similarity	66.7%: Pred. NO. 1.1e+02;				
Matches	4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;				
QY	7 TOEVKK 12				
DB	9 TQDIKK 14				
RESULT 2					
ID	GYRA_STRSH	STANDARD:	PRT:	21 AA.	
AC	P50071:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	01-OCT-1996 (Rel. 34, Last annotation update)				
DE	DNA GYRASE SUBUNIT A (EC 5.99.1.3) (FRAGMENT).				
GN	GYRA.				
OS	Streptomyces sphaeroides.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-NCIB 11891:				
RX	MEDLINE-93316846; PubMed-8392138;				
RA	Thiara A.S., Cundliffe E.:				
RT	"Expression and analysis of two gyrB genes from the novobiocin				
RT	producer, Streptomyces sphaeroides."				
RL	Mol. Microbiol. 8:495-506(1993).				

CC -1- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
CC -1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
CC OF DOUBLE-STRANDED DNA.
CC -1- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
CC ENZYME FORMS AN A2B2 TETRAMER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z17305; CAA78953.1; -
CC DR Topoisomerase: Isomerase; DNA-binding.
CC FT NON_TER 21 21
CC SEQUENCE 21 AA: 2203 MW: 5E2F9DEA8DB83697 CRC64:

Query Match 40.0%; Score 24; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 STVPAPRO 8
: 1111 :
DB 5 NTPVMPPEE 12

RESULT 3
ID IPPD_MOUSE STANDARD; PRT; 27 AA.
AC 060829;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DOPAMINE- AND CAMP-REGULATED NEURONAL PHOSPHOPROTEIN (DARPP-32)
DE (FRAGMENT).
GN PPPIR1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RX MEDLINE-96043524; PubMed-7485543;
RA Blau S., Daly L., Fienberg A., Teitelman G., Ehrlich M.E.;
RT "DARPP-32 promoter directs transgene expression to renal thick
RT ascending limb of loop of Henle.";
RL Am. J. Physiol. 269:F564-F570(1995).
CC -1- FUNCTION: INHIBITOR OF PROTEIN-PHOSPHATASE 1.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- PTM: DOPAMINE- AND CYCLIC AMP-REGULATED NEURONAL PHOSPHOPROTEIN
CC (BY SIMILARITY).
CC -----
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PHOSPHATASE INHIBITOR 1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U23160; AAA93223.1; -
CC DR Protein phosphatase inhibitor; Acetylation.
CC FT MOD_RES 1 1
CC FT NON_TER 27 27
CC SEQUENCE 27 AA: 3139 MW: 2FCB2C85F9458444 CRC64;

Query Match 38.3%; Score 23; DB 1; Length 27;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 STVPAPRO 8
: 1111 :
DB 12 SVRAPPQ 19

RESULT 4
ID Y161_TREPA STANDARD; PRT; 30 AA.
AC 083156;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL PROTEIN TP0161.
GN TP0161.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN-NICHOLES;
RX MEDLINE-98332770; PubMed-9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE001200; AAC65153.1; -
CC DR TIGR; TP0161;
KW Hypothetical protein.
SO SEQUENCE 30 AA: 3259 MW: 4B9A413A5498D15F CRC64;

Query Match 38.3%; Score 23; DB 1; Length 30;
Best Local Similarity 42.9%; Pred. No. 4.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

OY 1 STVPAP--TQEVKK 12
: 11111111 :
DB 6 AAPLRPKTQESER 19

RESULT 5
ID HM12_CAEEL STANDARD; PRT; 27 AA.
AC P17487;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HOMEROBOX PROTEIN CEH-12 (FRAGMENT).
GN CEH-12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-90245646; PubMed-1970877;
 RA Schaller D., Wilmann C., Spicher A., Mueller F., Tobler H.;
 RT "Cloning and analysis of three new homeobox genes from the nematode
 RT *Ceenorhabditis elegans*.";
 RL Nucleic Acids Res. 18:2033-2036(1990).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.ch).
 CC -----
 CC EMBL: X17076; CAA34928.1; -.
 DR PIR: S09504; S09504.
 DR HSSP: P02833; 110M.
 DR INTERPRO: IPR001356; -.
 DR PFAM: PF00046; homeobox; 1.
 DR PROSITE: PS00027; HOMEBOX_1; PARTIAL.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT NON_TER 1 1
 FT DNA_BIND <1 16 HOMEBOX.
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 3182 MW; FDAFDS16F3870A5 CRC64;

Query Match 36.7%; Score 22; DB 1; Length 27;
 Best Local Similarity 57.1%; Pred. No. 6e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 STPAPT 7
 Db 18 STPQST 24

RESULT 6
 ATP2_SPIOL
 ID ATP2_SPIOL STANDARD; PRT; 15 AA.
 AC P80083;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).
 GN ATPB OR ATP2.
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
 OC Caryophyllales; Chenopodiaceae; Spinacia.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-CV. MEDANIA; TISSUE-LEAF MESOPHYLL;
 RX MEDLINE-92209531; PubMed-1313368;
 RA Hammas B., Glaser E.;
 RT "Plant mitochondrial F1F1 ATP synthase. Identification of the
 RT individual subunits and properties of the purified spinach leaf
 RT mitochondrial ATP synthase.";
 RL Eur. J. Biochem. 205:409-416(1992).
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
 CC SUBUNIT.
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE_ALPHA/BETA CHAINS FAMILY.
 DR PIR: S21242; S21242.
 DR INTERPRO: IPR000194; -.
 DR PROSITE: PS00152; ATPASE_ALPHA_BETA; PARTIAL.

KM ATP synthetase; CF(1); Hydrogen ion transport;
 KW Hydrolyase; ATP-binding; Mitochondrion.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1295 MW; E5826224F63EE2CF CRC64;

Query Match 35.0%; Score 21; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 STPVA 5
 Db 11 STPLA 15

RESULT 7
 UC08_MAIZE
 ID UC08_MAIZE STANDARD; PRT; 15 AA.
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-COLEOPTILE;
 RA Touzel P., Riccardi F., Morin C., Damerwal C., Huet J.-C.,
 RA Penoulet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 38.8 KDA.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR MAIZE-2DPAGE: P80614; COLEOPTILE.
 DR MAIZEDB: 123934; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6A4BDF8D CRC64;

Query Match 35.0%; Score 21; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 PVPATOE 9
 Db 9 PVPVGE 15

RESULT 8
 RL6_VIBPR
 ID RL6_VIBPR STANDARD; PRT; 16 AA.
 AC Q56715;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L6 (FRAGMENT).
 GN RPLP.
 OS Vibrio proteolyticus (Aeromonas proteolytica).
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15338;
 RX MEDLINE-97149305; PubMed-8996113;
 RA Satterquist R.A., Smith G.K., Oakley T.H., Lee Y.H., Fox G.E.;
 RT "Sequence, overproduction and purification of Vibrio proteolyticus
 RT ribosomal protein L18 for in vitro and in vivo studies.";

RL Gene 183:237-242(1996).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
 CC LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE
 CC PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U38943; AABA1328.1; -
 CC DR INTERPRO: IPR002358; -
 CC DR PROSITE: PS00525; RIBOSOMAL_L6_1; PARTIAL.
 CC KW Ribosomal protein; rRNA-binding.
 CC FT NON_TER 1 1
 CC SO SEQUENCE 16 AA; 1935 MW; ABC1907BDF581B6C CRC64;

Query Match 35.0%; Score 21; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 TOEVRK 12
 I I I I
 Db 10 TREAKK 15

RESULT 9
 CH10_CLOPA STANDARD; PRT; 19 AA.
 AC P81338;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE 10 KDA CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (CP 31) (FRAGMENT).
 GN GROES.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 RN 11
 RP SEQUENCE.
 RC STRAIN-W5;
 RX MEDLINE-98291870; PubMed-9629918;
 RA Flengstrand R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SUPPRESSES
 CC THE ATPASE ACTIVITY OF THE LATTER (BY SIMILARITY).
 CC -1- SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
 CC DR INTERPRO: IPR001476; -
 CC DR PFAM: PF00166; cpn10; 1.
 CC DR PROSITE: PS00681; CHAPERONINS_CPN10; PARTIAL.
 CC KW Chaperone.
 CC FT NON_TER 19 19
 CC SO SEQUENCE 19 AA; 2026 MW; 766B9BD414E50A60 CRC64;

Query Match 35.0%; Score 21; DB 1; Length 19;
 Best Local Similarity 36.4%; Pred. No. 6.2e+02;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 TPVAPTOEVK 12
 I I I I
 Db 4 TPLGDNVYIKK 14

RESULT 10
 LAST_PIG STANDARD; PRT; 30 AA.
 AC P80171;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE LIM AND SH3 PROTEIN 1 (LASP-1) (CYSTEINE-RICH PEPTIDE ZF-1)
 DE (FRAGMENT).
 GN LASP1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN 11
 RP SEQUENCE.
 RC TISSUE-INTESTINE;
 RX MEDLINE-93145972; PubMed-8425549;
 RA Sillard R., Joernvall H., Carlquist M., Mutt V.;
 RT "Chemical assay for cyst(e)ine-rich peptides detects a novel
 RT intestinal peptide ZF-1, homologous to a single zinc-finger motif.";
 RL Eur. J. Biochem. 211:377-380(1993).
 RN 12
 RP STRUCTURE BY NMR.
 RX MEDLINE-96438771; PubMed-8841116;
 RA Hammarstrom A., Berndt K.D., Sillard R., Adermann K., Otting G.;
 RT "Solution structure of a naturally-occurring zinc-peptide complex
 RT demonstrates that the N-terminal zinc-binding module of the Laspl-1
 RT LIM domain is an independent folding unit.";
 RL Biochemistry 35:12723-12732(1996).
 CC -1- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.
 CC PIR: S28849; S28849.
 CC DR PDB: 1ZFO; 08-NOV-96.
 CC DR INTERPRO: IPR001781; -
 CC DR PFAM: PF00412; LIM_1.
 CC DR PROSITE: PS00478; LIM_DOMAIN_1; PARTIAL.
 CC DR PROSITE: PS00023; LIM_DOMAIN_2; 1.
 CC KW LIM motif; Metal-binding; zinc; Acetylation; 3D-structure.
 CC FT MOD_RES 1 1 ACETYLATION.
 CC FT DOMAIN 5 >30 LIM.
 CC FT NON_TER 30 30
 CC SO SEQUENCE 30 AA; 3517 MW; 042AB8FBE2314986 CRC64;

Query Match 35.0%; Score 21; DB 1; Length 30;
 Best Local Similarity 57.1%; Pred. No. 1e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 VAPTOEVK 10
 I I I I I
 Db 12 VYPLEVK 18

RESULT 11
 SPRC_RABIT STANDARD; PRT; 10 AA.
 ID SPRC_RABIT
 AC P36233;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SPARC (SECRETED PROTEIN ACIDIC AND RICH IN CYSTEINE) (OSTEONECTIN)
 DE (ON) (BASEMENT MEMBRANE PROTEIN BM-40) (FRAGMENT).
 GN SPARC.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN 11
 RP SEQUENCE.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-CARTILAGE;
 RX MEDLINE-94176562; PubMed-8130279;
 RA Chandrasekhar S., Harvey A.K., Johnson M.G., Becker G.W.;
 RT "Osteonectin/SPARC is a product of articular chondrocytes/cartilage
 RT and is regulated by cytokines and growth factors.";

RL Biochim. Biophys. Acta 1221:7-14(1994).
 CC -1- FUNCTION: APPEARS TO REGULATE CELL GROWTH THROUGH INTERACTIONS
 CC WITH THE EXTRACELLULAR MATRIX AND CYTOKINES. BINDS CALCIUM AND
 CC COPPER, SEVERAL TYPES OF COLLAGEN, ALBUMIN, THROMBOSPONDIN, PDGF
 CC AND CELL MEMBRANES. THERE ARE TWO CALCIUM BINDING SITES: A ACIDIC
 CC DOMAIN THAT BINDS 5 TO 8 CA++ WITH A LOW AFFINITY AND A EF-HAND
 CC LOOP THAT BINDS A CA++ ION WITH A HIGH AFFINITY.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN TISSUES
 CC UNDERGOING MORPHOGENESIS, REMODELING AND WOUND REPAIR.
 CC -1- INDUCTION: BY GROWTH FACTORS SUCH AS TGF-BETA, PDGF, IGF-1.
 CC -1- SIMILARITY: CONTAINS AN OSTEONECTIN-LIKE DOMAIN.
 DR PIR: S42762; S42762.
 DR INTERPRO: IPR001999; -.
 DR INTERPRO: IPR002048; -.
 DR PROSITE: PS00018; EF_HAND, PARTIAL.
 DR PROSITE: PS00612; OSTEONECTIN_1: PARTIAL.
 DR PROSITE: PS00613; OSTEONECTIN_2: PARTIAL.
 KM Extracellular matrix; Basement membrane; Glycoprotein;
 KW Calcium-binding; Copper.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1097 MW: DB5AB2672DDB06C6 CRC64:

Query Match 33.38; Score 20; DB 1; Length 10;
 Best Local Similarity 60.08; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 APR02 9
 11 11
 11 11
 Db 1 APOE 5

RESULT 12
 ODPF_CANFA
 ID ODPF_CANFA STANDARD; PRT; 13 AA.
 AC P49823;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT, SOMATIC FORM
 DE (EC 1.2.4.1) (PDH-E1-ALPHA TYPE 1) (FRAGMENT).
 GN PDHAF.
 OS Canis familiaris (Dog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEART;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
 CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
 CC COPIES OF THREE ENZYMAIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
 CC DIHYDROLIPOMIDE ACETYLTRANSFERASE (E2) & LIPOMIDE DEHYDROGENASE
 CC (E3).
 CC -1- CATALYTIC ACTIVITY: PYRUVATE + LIPOMIDE -> S-ACETYL-DIHYDRO-
 CC LIPOMIDE + CO(2).
 CC -1- COFACTOR: THIAMINE PYRROPHOSPHATE.
 CC -1- ENZYME REGULATION: E1 ACTIVITY IS REGULATED BY PHOSPHORYLATION
 CC (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVATION) OF THE ALPHA
 CC SUBUNIT (BY SIMILARITY).
 CC -1- SUBUNIT: Tetramer of two alpha and two beta subunits.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 DR HSC-2DPAGE; P49823; DOG.
 KM Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
 KM Mitochondrion; Phosphorylation.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA: 1510 MW: C97EEBF844085B19 CRC64:

Query Match 33.38; Score 20; DB 1; Length 13;
 Best Local Similarity 66.78; Pred. No. 6.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 TOEYVK 12
 11 11
 11 11
 Db 5 TFEIRK 10

RESULT 13
 RL10_CITFR
 ID RL10_CITFR STANDARD; PRT; 19 AA.
 AC P43448;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L10 (FRAGMENT).
 GN RPLJ.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Citrobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=771;
 RA Zhyvoloup A.N.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X74448; CA52459.1; -.
 DR INTERPRO: IPR002363; -.
 DR PROSITE: PS01109; RIBOSOMAL_L10: PARTIAL.
 KM Ribosomal protein.
 FT INIT_MET 0 BY SIMILARITY.
 FT NON_TER 19 19
 FT SEQUENCE 19 AA: 2026 MW: E20A02CD7851DB16 CRC64;

Query Match 33.38; Score 20; DB 1; Length 19;
 Best Local Similarity 55.68; Pred. No. 9.4e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 VAPTOEVK 12
 11 11
 11 11
 Db 11 VAEVSEVAK 19

RESULT 14
 RL10_PROVU
 ID RL10_PROVU STANDARD; PRT; 20 AA.
 AC P51411;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L10 (FRAGMENT).
 GN RPLJ.
 OS Proteus vulgaris.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Proteus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Zhyvoloup A.N.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: X74446; CAA52457.1; -
 DR INTERPRO: IPR002363; -
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2083 MW; 76520A02CD7851DB CRC64;

Query Match 33.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 55.6%; Pred. No. 9.9e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 VAPTOEVKK 12
 || ||
 DB 11 VAEVSEVAK 19

RESULT 15
 RL10_KLEPN
 ID RL10_KLEPN STANDARD; PRT; 22 AA.
 AC P41190;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L10 (FRAGMENT).
 GN RPLJ
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NCTC 5054;
 RA Zhyvoloup A.N.;
 RL Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: X74445; CAA52456.1; -
 DR PIR: S35975; S35975.
 DR PIR: S35976; S35976.
 DR INTERPRO: IPR002363; -
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT NON_TER 22 22
 SQ SEQUENCE 22 AA; 2268 MW; 113D96520A02CD78 CRC64;

Query Match 33.3%; Score 20; DB 1; Length 22;
 Best Local Similarity 55.6%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 VAPTOEVKK 12
 || ||
 DB 11 VAEVSEVAK 19

THIS PAGE BLANK (USPTO)

This Page Blank (uspic,

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:06:29 ; Search time 58.16 Seconds

(without alignments)
24.183 Million cell updates/sec

Title: US-09-372-036-30

Perfect score: 60
Sequence: 1 STPVAPPTQEVKK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 10868

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	48.3	23	11	Q63334
2	29	48.3	29	12	Q91011
3	29	48.3	29	12	Q91010
4	27	45.0	21	10	Q42417
5	27	45.0	21	10	Q42501
6	27	45.0	21	10	Q95756
7	26	43.3	21	10	Q41559
8	26	43.3	21	10	Q41564
9	26	43.3	23	12	Q905P0
10	26	43.3	24	12	Q85618
11	26	43.3	27	10	Q958L3
12	25	41.7	22	1	Q9UW19
13	25	41.7	22	13	Q9PS65
14	25	41.7	23	11	Q35829
15	25	41.7	27	2	Q9R5D8
16	25	41.7	29	12	Q9QMX9
17	25	41.7	30	12	Q9QMY0
18	24.5	40.8	30	1	Q9V2V2
19	24.5	40.8	30	2	Q52184

20	24	40.0	17	5	Q9TWR3	Q9TWR3 trypanosoma
21	24	40.0	19	2	Q9RBY1	Q9RBY1 pseudomonas
22	24	40.0	20	10	Q9S8Y0	Q9S8Y0 phleum prat
23	24	40.0	21	10	Q41565	Q41565 triticum ae
24	24	40.0	24	8	Q37085	Q37085 iris tenax.
25	24	40.0	24	8	Q37804	Q37804 iris chryso
26	24	40.0	24	8	Q37829	Q37829 iris hartwe
27	24	40.0	24	8	Q32448	Q32448 iris chryso
28	24	40.0	24	8	Q32466	Q32466 iris prisma
29	24	40.0	24	8	Q32444	Q32444 iris bracte
30	24	40.0	24	8	Q32452	Q32452 iris fernal
31	24	40.0	24	8	Q32453	Q32453 iris hartwe
32	24	40.0	24	8	Q37824	Q37824 iris dougla
33	24	40.0	24	8	Q32467	Q32467 iris purdyi
34	24	40.0	24	8	Q32458	Q32458 iris innomi
35	24	40.0	24	8	Q32454	Q32454 iris hartwe
36	24	40.0	24	8	Q32460	Q32460 iris macros
37	24	40.0	24	8	Q32461	Q32461 iris munzli
38	24	40.0	24	8	Q32445	Q32445 iris bracte
39	24	40.0	24	8	Q32455	Q32455 iris hartwe
40	24	40.0	24	8	Q32459	Q32459 iris macros
41	24	40.0	24	8	Q32462	Q32462 iris munzli
42	24	40.0	24	8	Q32471	Q32471 iris tenuis
43	24	40.0	24	11	Q9WVE6	Q9WVE6 mus musculi
44	24	40.0	25	13	Q9PSB2	Q9PSB2 xenopus bor
45	24	40.0	27	12	Q911S7	Q911S7 hepatis c

ALIGNMENTS

RESULT 1
ID 063334 PRELIMINARY: PRT: 23 AA.

AC Q63334; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ALPHA-2-MACROGLOBULIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-WISTAR.
RX MEDLINE=65207604; PubMed=42581948;
RA Northmann W., Heisig M., Kunz D., Heinrich P.C.;
RT "Molecular cloning of cDNA sequences for rat alpha 2-macroglobulin and
RT measurement of its transcription during experimental inflammation.";
RL J. Biol. Chem. 260:6200-6205(1985).
DR EMBL: M64369; AAA4594.1; -;
DR INTERPRO: IPR001599; -;
DR PRAM: PF00207; A2M; 1;
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2526 MW; E2D721FBI23876 CRC64;.

Query Match 48.3%; Score 29; DB 11; Length 23;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 2
ID 091011 PRELIMINARY: PRT: 29 AA.
AC Q91011;
DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE TAT PROTEIN (FRAGMENT).
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT 17;
 RA Yamada T., Iwamoto A.;
 RT nonprogressors and progressors of human immunodeficiency virus type 1
 RT Infection.;
 RL Arch. Virol. 145:1021-1027(2000).
 DR EMBL: AB034453; BAA93910.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA: 3013 MM: 83CFF93D51DA7255 CRC64;

Query Match
 Best Local Similarity 48.3%; Score 29; DB 12; Length 29;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PVAPTOEVKK 12
 DB 9 PTGPTESKKK 18

RESULT 3
 ID 091010 PRELIMINARY; PRT; 29 AA.
 AC 091010;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE TAT PROTEIN (FRAGMENT).
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 NCBI_Taxid=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT 17;
 RA Yamada T., Iwamoto A.;
 RT *Comparison of proviral accessory genes between long-term
 RT nonprogressors and progressors of human immunodeficiency virus type 1
 RT Infection.;
 RL Arch. Virol. 145:1021-1027(2000).
 DR EMBL: AB034454; BAA93911.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA: 3085 MM: 83CFF93D51DA7255 CRC64;

Query Match
 Best Local Similarity 48.3%; Score 29; DB 12; Length 29;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PVAPTOEVKK 12
 DB 9 PTGPTESKKK 18

RESULT 4
 ID 042417 PRELIMINARY; PRT; 21 AA.
 AC 042417;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
 GN HSP16.9-17LC3.
 OS Triticum aestivum (wheat).
 NCBI_Taxid=4565;

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 NCBI_Taxid=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MUSTANG;
 RA Joshi C.P., Nguyen H.T.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L37070; AAA51390.1; -.
 DR EMBL: L37068; AAA51388.1; -.
 DR EMBL: L37069; AAA51389.1; -.
 KW Heat shock.
 FT NON_TER 1 1
 SQ SEQUENCE 21 AA: 2266 MM: 489524EDE9A0527F CRC64;

Query Match
 Best Local Similarity 45.0%; Score 27; DB 10; Length 21;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TPVAPTOEVKK 12
 DB 1 TVTVPKAEVKK 11

RESULT 5
 ID 042501 PRELIMINARY; PRT; 21 AA.
 AC 042501;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
 GN HSP16.9-5LC1.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 NCBI_Taxid=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MUSTANG;
 RA Joshi C.P., Nguyen H.T.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L37075; AAA51395.1; -.
 DR EMBL: L37067; AAA51387.1; -.
 KW Heat shock.
 FT NON_TER 1 1
 SQ SEQUENCE 21 AA: 2223 MM: 522524F029A0527F CRC64;

Query Match
 Best Local Similarity 45.0%; Score 27; DB 10; Length 21;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TPVAPTOEVKK 12
 DB 1 TVTVPKAEVKK 11

RESULT 6
 ID 095756 PRELIMINARY; PRT; 21 AA.
 AC 095756;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
 GN HSP16.9-8LC3 OR HSP16.9-14LC1 OR HSP16.9-2LC2 OR HSP16.9-3LC1.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 NCBI_Taxid=4565;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-MUSTANG;
 RA Joshi C.P., Nguyen H.T.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L37064; AAA51384.1; -
 RT "Differential display mediated rapid cloning and sequencing of the 3' region of several members of a large multigene family."
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L37076; AAA51396.1; -
 DR EMBL: L37066; AAA51386.1; -
 DR EMBL: L37072; AAA51392.1; -
 DR EMBL: L37073; AAA51393.1; -
 KM Heat shock.
 FT NON_TER
 SQ SEQUENCE 21 AA; 2224 MW; 522524EDE9A0527F CRC64;

Query Match 45.0%; Score 27; DB 10; Length 21;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TPVAPTOEVKK 12
 Db 1 TVTVPKAEVKK 11

RESULT 7
 Q41559 PRELIMINARY; PRT; 21 AA.
 ID Q41559;
 AC Q41559;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
 GN HSP16.9-10LC1.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MUSTANG;
 RA Joshi C.P., Nguyen H.T.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L37061; AAA51382.1; -
 KM Heat shock.
 FT NON_TER
 SQ SEQUENCE 21 AA; 2269 MW; 522524F03B33376B CRC64;

Query Match 43.3%; Score 26; DB 10; Length 21;
 Best Local Similarity 45.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 TPVAPTOEVKK 12
 Db 1 TVTVPKAEVKK 11

RESULT 8
 Q41564 PRELIMINARY; PRT; 21 AA.
 ID Q41564;
 AC Q41564;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
 GN HSP16.9-12LC2.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MUSTANG;

RA Joshi C.P., Nguyen H.T.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L37064; AAA51384.1; -
 RT "Differential display mediated rapid cloning and sequencing of the 3' region of several members of a large multigene family."
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L37076; AAA51396.1; -
 DR EMBL: L37066; AAA51386.1; -
 DR EMBL: L37072; AAA51392.1; -
 DR EMBL: L37073; AAA51393.1; -
 KM Heat shock.
 FT NON_TER
 SQ SEQUENCE 21 AA; 2255 MW; 536024F03B33376B CRC64;

Query Match 43.3%; Score 26; DB 10; Length 21;
 Best Local Similarity 45.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 TPVAPTOEVKK 12
 Db 1 TVTVPKAEVKK 11

RESULT 9
 Q9QSP0 PRELIMINARY; PRT; 23 AA.
 ID Q9QSP0;
 AC Q9QSP0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE L. PROTEIN (FRAGMENT).
 GN L.
 OS Australian bat lyssavirus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 NCBI_TaxID=90961;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INSECTORIOUS ISOLATE;
 RA Gould A.R., Kattenbelt J.A., Hyatt A.D., Gumley S.G., Lunt R.A.;
 RT "Characterisation of a variant of Australian Bat Lyssavirus isolated from an insectivorous bat and comparison to virus isolates from Pteropid bats."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF081020; AAD47900.1; -
 FT NON_TER
 SQ SEQUENCE 23 AA; 2599 MW; 7B584A2225E76530 CRC64;

Query Match 43.3%; Score 26; DB 12; Length 23;
 Best Local Similarity 55.6%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PVAPTOEVKK 11
 Db 14 PVPEPEELK 22

RESULT 10
 Q85618 PRELIMINARY; PRT; 24 AA.
 ID Q85618;
 AC Q85618;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE RAV-2 PROVIRAL DNA, C-MYC (AA 44-67), ALLELE LL3 (FRAGMENT).
 OS Avian leukosis virus.
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 NCBI_TaxID=11864;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8414799; PubMed=6322173;
 RA Westaway D., Payne G., Varmus H.E.;
 RT "Proviral deletions and oncogene base-substitutions in insertionally mutagenized c-myc alleles may contribute to the progression of avian bursal tumors."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:843-847(1984).
 DR EMBL: K01439; AAA51600.1; -
 FT NON_TER

FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2679 MW; 93F59F2D3B24E527 CRC64;

Query Match
Best Local Similarity 43.3%; Score 26; DB 12; Length 24;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 PVAPTOEVKK 12
Db 2 PPAPSEDVKK 11

RESULT 11

O9S8L3 PRELIMINARY; PRT; 27 AA.
AC O9S8L3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE FLAVODOXIN I (FRAGMENT).
OS Chlorocella fusca.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlorococcales;
OC Scenedesmeaceae; Scenedesmus.
OX NCBI_TaxID=3073;
RN 11
RP SEQUENCE.
RA MEDLINE=95031921; PubMed=7945206;
RA Pelaez M.L., Ayora S., Inda L.A., Gomez-Moreno C.;
RT Isolation and characterization of two different flavodoxins from the
KT eukaryote Chlorocella fusca."
RL Biochem. J. 302:807-811(1994).
DR HSSP; P14070; 2FCR.
DR INTERPRO; IPR001226;
DR PFAM; PF00258; flavodoxin.1.
DR PROSITE; PS00201; FLAVODOXIN; UNKNOWN.1.
SQ SEQUENCE 27 AA; 2780 MW; F9A77B03B82D298E CRC64;

Query Match
Best Local Similarity 43.3%; Score 26; DB 10; Length 27;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 STVPAPTOEV 10
Db 7 STATGKTOEV 16

RESULT 12

O9UW19 PRELIMINARY; PRT; 22 AA.
AC O9UW19;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 5 KDA FLAGELLIN (FRAGMENT).
OS Methanospirillum hungatei.
OC Archaea; Euryarchaeota; Methanomicrobiales; Methanomicrobiaceae;
OC Methanospirillum.
OX NCBI_TaxID=2203;
RN 11
RP SEQUENCE.
RX MEDLINE=95095917; PubMed=8002572;
RA Faguy D.M., Koval S.F., Jarrell K.F.;
RT Physical characterization of the flagella and flagellins from
RT Methanospirillum hungatei."
RL J. Bacteriol. 176:7491-7498(1994).
SQ SEQUENCE 22 AA; 2360 MW; 168505F27B4F79E5 CRC64;

Query Match
Best Local Similarity 41.7%; Score 25; DB 1; Length 22;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 VAPTOEVKK 11
Db 8 LVPTKVK 15

RESULT 13

O9PS65 PRELIMINARY; PRT; 22 AA.
AC O9PS65;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE HISTONE H1B.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN 11
RP SEQUENCE.
RX MEDLINE=92082492; PubMed=1747124;
RA Davie J.R., Delcuve G.P.;
RT "Characterization and chromatin distribution of the H1 histones and
RT high-mobility-group non-histone chromosomal proteins of trout liver
and hepatocellular carcinoma."
RL Biochem. J. 280:491-497(1991).
SQ SEQUENCE 22 AA; 2132 MW; 3E9038F68189AE3 CRC64;

Query Match
Best Local Similarity 41.7%; Score 25; DB 13; Length 22;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 TPVAPTOEVKK 12
Db 3 TAAAPAPKAKK 13

RESULT 14

O3S829 PRELIMINARY; PRT; 23 AA.
AC O3S829;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)
DE LAMIN A (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;
RA Tiwari B., Parnaik V.K.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y15465; CAA75647.1; -.
FT NON_TER 23
SQ SEQUENCE 23 AA; 2435 MW; 4E27DD477E1925FE CRC64;

Query Match
Best Local Similarity 41.7%; Score 25; DB 11; Length 23;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 STVPAP 6
Db 18 STPMSP 23

RESULT 15
O9R5D8 PRELIMINARY; PRT; 27 AA.
ID O9R5D8

AC Q9R5D8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE FIBROBLAST-ACTIVATING FACTOR (FRAGMENT).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; CBG group; Bacteroidaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93138782; PubMed=8380795;
 RA Mihara J., Holt S.C.;
 RT "Purification and characterization of fibroblast-activating factor
 RL isolated from Porphyromonas gingivalis W50.";
 RL Infect. Immun. 61:588-595(1993).
 SQ SEQUENCE 27 AA; 2841 MW; C06B390BA2925337 CRC64;

Query Match 41.78; Score 25; DB 2; Length 27;
 Best Local Similarity 60.0%; Pred. NO. 6.5e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 STPVAPTOEV 10
 DB 7 STPEAVTKTV 16

Search completed: February 13, 2001, 13:06:30
 Job time: 312 sec

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:02:02 ; Search time 44.34 Seconds
(without alignments)
7.712 Million cell updates/sec

Title: US-09-372-036-31
Perfect score: 51
Sequence: 1 PVAPRQEVKK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 151408

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/geneseq/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/AA2000.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	14	AA1973
2	51	100.0	12	14	AA1972
3	51	100.0	21	16	R73891
4	36	70.6	7	16	R73903
5	32	62.7	6	14	R54615
6	32	62.7	9	14	AA15168
7	32	62.7	20	14	AA15159
8	32	62.7	20	20	W78130
9	29	56.9	29	7	P61306
10	28	54.9	7	19	Y21365
11	28	54.9	11	16	R75105
12	28	54.9	11	17	W10057

13	28	54.9	27	17	W01470	Agammaglobulinemia
14	28	54.9	28	20	Y03800	Murine LckBPI pept
15	27	52.9	9	17	W07056	Synthetic peptide
16	27	52.9	15	11	Y17929	Synthetic peptide
17	27	52.9	15	14	R34237	HTLV-II envelope g
18	27	52.9	15	16	R79629	Endocarditis speci
19	27	52.9	20	15	R46816	Phytase derived pe
20	27	52.9	21	16	R73894	Listeria monocyog
21	27	52.9	28	15	R49685	Sequence of trypti
22	26	51.0	15	19	W75624	M. tuberculosis 30
23	26	51.0	15	19	W75625	M. tuberculosis 30
24	26	51.0	15	19	W46779	Species-specific a
25	26	51.0	27	18	W10027	Sporozoite attachm
26	26	51.0	30	13	R24138	Precursor region o
27	26	51.0	30	21	Y69503	C-terminus of MMLV
28	25	49.0	10	20	W95056	Urokinase peptide
29	25	49.0	15	15	R46793	Phytase derived pe
30	25	49.0	16	18	W38995	HTLV-PX-related pe
31	25	49.0	17	9	P81134	Control peptide.
32	25	49.0	17	16	R71630	Transactivating pr
33	25	49.0	19	17	R95686	HTLV-1 p40(tax) pr
34	25	49.0	20	15	R61281	Tax protein fragme
35	25	49.0	20	16	R74361	Sequence of the fu
36	25	49.0	20	19	W41195	Linking sequence f
37	25	49.0	21	9	P81672	Plasminogen - tiss
38	25	49.0	21	18	W22737	Puumala virus nucl
39	25	49.0	27	11	R05105	HIV gag protein re
40	25	49.0	30	18	W30790	HIV-1 p24 protein
41	24	47.1	9	14	R46520	Amino acid sequenc
42	24	47.1	9	20	Y53518	HIV-derived lipope
43	24	47.1	9	20	Y26859	Peptide fragment o
44	24	47.1	9	20	Y26859	
45	24	47.1	10	11	R07909	

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	AA1973	51	100.0	10	14	AA1973
2	AA1972	51	100.0	12	14	AA1972
3	R73891	36	70.6	7	16	R73891
4	R73903	32	62.7	6	14	R73903
5	R54615	32	62.7	9	14	R54615
6	AA15168	32	62.7	20	14	AA15168
7	AA15159	32	62.7	20	14	AA15159
8	W78130	32	62.7	20	20	W78130
9	P61306	29	56.9	29	7	P61306
10	Y21365	28	54.9	7	19	Y21365
11	R75105	28	54.9	11	16	R75105
12	W10057	28	54.9	11	17	W10057

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (Partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
 |||||
 Db 1 pvaptgevk 10

RESULT 2

R45172 R45172 standard; Protein; 12 AA.

XX R45172:

XX 16-JUN-1994 (first entry)

XX *Listeria* p60 peptide epitope.

XX *Listeria* monocytogenes; antibodies; immunoassay; conjugate.

XX Synthetic.

XX DE4318450-A.

XX 16-DEC-1993.

XX 03-JUN-1993; 93DE-4318450.

XX 11-JUN-1992; 92DE-4219111.

XX 25-NOV-1992; 92DE-4239567.

XX (MERC) MERCK PATENT GMBH.

XX Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;
 PI Hofmann G, Buhert A, Goebel W, Koehler S;

XX WPI: 1993-406956/51.

XX New primers for PCR detection of *Listeria* - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection

XX Disclosure: Fig 2; 19pp; German.

XX The sequence is that of a *Listeria* p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of *Listeria* by immunoassay (Partic. ELISA). It may be used as
 CC part of a method that allows determination of individual *Listeria*
 CC species, esp. *L. monocytogenes*.
 XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 51; DB 14; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
 |||||
 Db 3 pvaptgevk 12

RESULT 3
 R73891 R73891 standard; peptide; 21 AA.

XX R73891:

XX 05-DEC-1995 (first entry)

XX *Listeria* monocytogenes protein p60 precursor peptide 144-164.

XX *Listeria* monocytogenes; protein p60 precursor; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
 KW viral; peptide 144-164.

XX *Listeria* monocytogenes.

XX WO9509232-A.

XX 06-APR-1995.

XX 28-SEP-1994; 94WO-CA00516.

XX 28-SEP-1993; 93US-0127499.

XX (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.

XX Sharma LR, Van Alstyne D;

XX WPI: 1995-147431/19.

XX New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis

XX Claim 34; Page 74; 98pp; English.

XX R73913 is the *Listeria* monocytogenes protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in R73891-R73894 and R73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.

XX Sequence 21 AA;

Query Match 100.0%; Score 51; DB 16; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
 |||||
 Db 5 pvaptgevk 14

RESULT 4

R73903 R73903 standard; peptide; 7 AA.

XX R73903:

XX 05-DEC-1995 (first entry)

XX *Listeria* monocytogenes protein p60 precursor peptide 151-157.
 KW *Listeria* monocytogenes; protein p60 precursor; vaccine;
 KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
 KW immunoassay; diagnosis; treatment; prophylactic; bacterial;

KM viral: peptide 151-157.
 OS Listeria monocytogenes.
 XX MO9509232-A.
 XX 06-APR-1995.
 PD 28-SEP-1994; 94MO-CA00516.
 XX 28-SEP-1993; 93US-0127499.
 PR (SHAR/) SHARMA L R.
 PA (VALS/) VAN ALSTYNE D.
 XX Sharma LR, Van Alstyne D;
 PI WPI; 1995-147431/19.
 DR
 XX
 PT New peptide(s) and corresp. antibodies for the treatment of
 PT meningitis - the peptide(s) corresp. to homologous antigenic
 PT sites on bacterial and viral agents and on chemokine(s), used for
 PT detecting and preventing meningitis
 XX
 PS Claim 35; Page 76; 98pp; English.
 XX
 CC R73913 is the Listeria monocytogenes protein p60 precursor. It
 CC contains the meningitis related antigenic sequences (MRHAS) claimed
 CC in R73891-R73894 and R73903-R73906, which are recognised by a
 CC monoclonal antibody from the hybridoma Rubella virus (RV)-1. The
 CC claimed MRHAS peptides may be used in immunoassays to diagnose the
 CC presence of bacterial and/or viral meningitis agents in a sample,
 CC or in prophylactic and therapeutic meningitis treatments. The
 CC peptides may also be used as vaccines against meningitis.
 XX
 SO Sequence 7 AA:

 Query Match 70.6%; Score 36; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2,1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 PTOEVKK 10
 |||||
 Db 1 ptgevkk 7

 RESULT 5
 R54615 R54615 standard; Protein; 6 AA.
 XX
 AC R54615;
 XX
 DT 16-JUN-1994 (first entry)
 DE Listeria p60 peptide epitope.
 XX
 KM Listeria monocytogenes; antibodies; immunoassay; conjugate.
 OS Synthetic.
 XX
 PN DE4318450-A.
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;

PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure; Page 3; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 XX
 SO Sequence 6 AA:

 Query Match 62.7%; Score 32; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2,1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 PVAPFQ 6
 |||||
 Db 1 pvapftq 6

 RESULT 6
 R45168 R45168 standard; Protein; 9 AA.
 XX
 ID R45168;
 AC R45168;
 XX
 DT 16-JUN-1994 (first entry)
 DE Listeria p60 peptide epitope.
 XX
 KM Listeria monocytogenes; antibodies; immunoassay; conjugate.
 OS Synthetic.
 XX
 PN DE4318450-A.
 PD 16-DEC-1993.
 XX
 PF 03-JUN-1993; 93DE-4318450.
 XX
 PR 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Bubert A, Goebel W, Koehler S;
 XX
 DR WPI; 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 XX
 PS Disclosure; Fig 2; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 XX
 SO Sequence 9 AA:

Query Match 62.7%; Score 32; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPQ 6
 DB 4 PVAPQ 9
 111111

RESULT 7
 ID R45159 standard; Protein: 20 AA.
 AC R45159;
 XX
 XX 16-JUN-1994 (first entry)
 DE Listeria p60 peptide epitope.
 XX Listeria monocytogenes; antibodies; immunoassay; conjugate.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT 1..7
 FT Region /note="opt. 0-7 amino acid residues"
 FT 14..20
 FT /note="opt. 0-7 amino acid residues"

DE4318450-A.
 PN 16-DEC-1993.
 PD
 XX
 XX 03-JUN-1993; 93DE-4318450.
 PE
 XX
 XX 11-JUN-1992; 92DE-4219111.
 PR 25-NOV-1992; 92DE-4239567.
 XX
 XX (MERE) MERCK PATENT GMBH.
 PA
 PI Schubert P, Neumann S, Pawelzik M, Linxweller W, Burger C;
 PI Hofmann G, Buber A, Goebel W, Koehler S;
 XX
 DR WPI: 1993-406956/51.
 XX
 PT New primers for PCR detection of Listeria - including individual
 PT species, also new peptide(s) for raising antibodies for
 PT immunochemical detection
 PT
 XX
 PS Claim 3; Page 4; 19pp; German.
 XX
 CC The sequence is that of a Listeria p60 peptide epitope which
 CC which may be used in the prodn. of antibodies for the detection
 CC of Listeria by immunoassay (partic. ELISA). It may be used as
 CC part of a method that allows determination of individual Listeria
 CC species, esp. L. monocytogenes.
 CC
 XX
 SQ Sequence 20 AA;

Query Match 62.7%; Score 32; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPQ 6
 DB 8 PVAPQ 13
 111111

RESULT 8
 ID W78130 standard; Protein: 27 AA.
 XX

AC W78130;
 XX
 XX 13-APR-1999 (first entry)
 DE
 XX Human secreted protein encoded by gene 5 clone HPBD36.
 XX
 XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 27
 FT /label= unknown

W09856804-A1.
 PD 17-DEC-1998.
 XX
 XX 11-JUN-1998; 98WO-US12125.
 PF
 XX
 XX 02-OCT-1997; 97US-0061060.
 PR 13-JUN-1997; 97US-0049547.
 PR 13-JUN-1997; 97US-0049548.
 PR 13-JUN-1997; 97US-0049549.
 PR 13-JUN-1997; 97US-0049550.
 PR 13-JUN-1997; 97US-0049606.
 PR 13-JUN-1997; 97US-0049607.
 PR 13-JUN-1997; 97US-0049608.
 PR 13-JUN-1997; 97US-0049609.
 PR 13-JUN-1997; 97US-0049610.
 PR 13-JUN-1997; 97US-0049611.
 PR 13-JUN-1997; 97US-0050566.
 PR 13-JUN-1997; 97US-0050901.
 PR 13-JUN-1997; 97US-0052889.
 PR 08-JUL-1997; 97US-0051819.
 PR 18-AUG-1997; 97US-0055984.
 PR 12-SEP-1997; 97US-0058665.
 PR 12-SEP-1997; 97US-0058668.
 PR 12-SEP-1997; 97US-0058669.
 PR 12-SEP-1997; 97US-0058750.
 PR 12-SEP-1997; 97US-0058871.
 PR 12-SEP-1997; 97US-0058972.
 PR 12-SEP-1997; 97US-0058975.
 PR 02-OCT-1997; 97US-0060834.
 PR 02-OCT-1997; 97US-0060841.
 PR 02-OCT-1997; 97US-0060844.
 PR 02-OCT-1997; 97US-0060865.
 PR 02-OCT-1997; 97US-0061059.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Brewer LA, Ehner R, Ferrie AM, Feng P, Greene JM, Lafleur DM;
 PI Moore PA, NI J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
 PI Yu GL;
 XX
 DR WPI: 1999-080881/07.
 DR N-PSDB; X04315.
 XX
 XX
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 11; Page 266; 380pp; English.
 XX
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate

CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. X04302) for increasing the stability of the fused protein
 CC as compared to the human protein only.
 CC The invention relates to 86 novel genes and their fragments (nucleic acid
 CC sequences: X04311-X04410; amino acid sequences W78126-W78225) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 86 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X04311 for described
 CC uses).

XX Sequence 27 AA;

Query Match 62.7%; Score 32; DB 20; Length 27;
 Best Local Similarity 60.0%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 PVAPTOEVKK 10
 ||||: ||
 Db 9 pvpptetsqk 18

RESULT 9
 P61306
 ID P61306 standard; Protein: 29 AA.

AC P61306;

DT 05-JUN-1991 (first entry)

DE Trans-acting transcription factor of the HTLV-III ARV genome exon 2.

KM Viral surface glycoprotein; vaccine.

OS Human T-cell lymphotropic virus.

PN W08505636-A.

PD 19-DEC-1985.

PF 24-MAY-1985; 85WO-US00985.

PR 25-MAY-1984; 84US-0614297.

PR 06-DEC-1985; 85US-0806263.

PA (DANA-) DANA-FARBER CANCER.

PI Haseltine WA, Sodroski JG, Rosen CA;

WP1: 1986-006897/01.

DR N-PSDB; N60931.

PT System for increasing gene expression in host cells - comprises
 PT vector including cis-acting element and trans acting segment of
 PT retro-virus DNA.

PS Disclosure; Fig 5; 67pp; English.

CC Placing the trans-acting sequence in a cell with an expression
 CC vector carrying the gene to be expressed and a cis-acting element,
 CC allows for the increased yield of the product. The system is
 CC especially useful in the isolation of viral surface proteins as
 CC antigens or vaccines.

XX Sequence 29 AA;

Query Match 56.9%; Score 29; DB 7; Length 29;
 Best Local Similarity 50.0%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 PVAPTOEVKK 10
 ||||: ||
 Db 9 pvpptetsqk 18

RESULT 10
 Y21365
 ID Y21365 standard; Protein: 7 AA.

AC Y21365;

DT 22-JUL-1999 (first entry)

DE Human HUPF-I mutant protein fragment 17.

KW Human, beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-I;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.

OS Synthetic.

OS Homo sapiens.

PN W09845322-A2.

PD 15-OCT-1998.

PF 02-APR-1998; 98WO-1B00705.

PR 10-APR-1997; 97US-0043163.

PA (UYUT-) RIJKSUNIV UTRECHT.

PA (ROYA-) ROYAL NETHERLANDS ACADEMIES OF SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PI Burbach JPH, Grosveld FG, van Leeuwen FW;

WP1: 1998-609901/51.

DR N-PSDB; X75768.

PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA

PS Disclosure; Figure 17; 258pp; English.

CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-I, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.

XX Sequence 7 AA;

Query Match 54.9%; Score 28; DB 19; Length 7;
Best Local Similarity 83.3%; Pred. No. 2.1e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAPTO 6
11111:
Db 2 pvaplr 7

RESULT 11
R75105
ID R75105 standard; peptide: 11 AA.

AC R75105;

DT 01-FEB-1996 (first entry)

DE Recombinant bile salt-activated lipase C-terminal repeat 7.

XX Bile salt activated lipase; BAL; C-terminal repeat.

OS Synthetic.

PN JP07111891-A.

PD 02-MAY-1995.

PF 30-SEP-1993; 93JP-0245079.

PR 30-SEP-1993; 93JP-0245079.

PA (MEIP) MEIJI MILK PROD CO LTD.

DR WPI; 1995-196318/26.

DR N-PSDB: Q90576.

PT New recombinant bile salt-activated lipase(s), DNA encoding them
and vectors - useful for high level expression of the lipase(s) by
fermenter-culturing.

PS Claim 1; Page 9; 31pp; Japanese.

CC New lipases are ones in which 1-15 repeats of any of the sequences
R75099-R75105 (encoded by Q90570-Q90576) are attached to the C-
terminus of the bile salt-activated lipase (BAL) of sequence R75098
(encoded by Q90569) and/or in which the amino acid sequence SMTGS
(encoded by Q90578) is attached to the N-terminus of the BAL. The
recombinant lipases can be produced by fermentation in transformed
Pichia pastoris GS 115 host cells.

SQ Sequence 11 AA;

Query Match 54.9%; Score 28; DB 16; Length 11;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTOEVRK 10
11111:
Db 1 pvppldske 10

RESULT 12

W10057
ID W10057 standard; Protein: 11 AA.

AC W10057;

DT 28-FEB-1997 (first entry)

XX 11 amino acid C-terminal repeat sequence of recombinant human BAL.

DE BAL: bile salt-activated lipase; C-terminal repeat; recombinant;
KW high yield; Pichia pastoris GS115; plasmid; transformation; PHIL301;
 fermentation.

OS Homo sapiens.

PN JP08228779-A.

PD 10-SEP-1996.

PF 28-FEB-1995; 95JP-0039889.

PR 28-FEB-1995; 95JP-0039889.

PA (MEIP) MEIJI MILK PROD CO LTD.

DR WPI; 1996-459145/46.

PT High yield expression of recombinant bile salt activated lipase
in plasmid PHIL301 transformed Pichia pastoris GS115

PS Disclosure; Page 8; 12pp; Japanese.

CC W10051-W10057 are seven possible sequences that may feature in a
C-terminal repeat region, consisting of 16 repeated sequences of 11
amino acids, of human recombinant bile salt-activated lipase (BAL),
see W10050. The invention is directed to the recombinant production of
CC BAL at a high yield. Recombinant BAL, contg. the C-terminal repeats, was
expressed in Pichia pastoris that had been transformed by plasmid
CC PHIL301 and cultured at 15-30 deg.C. at not more than 20% dissolved
oxygen. This process resulted in a markedly high yield of BAL enzyme.

SQ Sequence 11 AA;

Query Match 54.9%; Score 28; DB 17; Length 11;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTOEVRK 10
11111:
Db 1 pvppldske 10

RESULT 13

W01470
ID W01470 standard; Protein: 27 AA.

AC W01470;

DT 05-FEB-1997 (first entry)

DE Agammaglobulinemia tyrosine kinase fragment 3.

KW agammaglobulinemia; tyrosine kinase; sex-linked; analysis;
 gene therapy; diagnosis; carrier.

OS Homo sapiens.

PN JP08205898-A.

PD 13-AUG-1996.

PF 01-FEB-1995; 95JP-0034715.

PR 01-FEB-1995; 95JP-0034715.

PA (MITP) MITSUBISHI YUKA BCL KK.

DR WPI; 1996-419829/42.

DR N-PSDB: T44529.
 XX DNA fragment contg. gene involved in sex-linked agammaglobulinemia -
 PT useful for diagnosing an XLA carrier and for gene therapy
 XX
 PS Claim 1; Page 9; 15pp; Japanese.
 XX
 CC The agammaglobulinemia tyrosine kinase (ATK) gene is involved in sex-
 CC linked agammaglobulinemia (XLA). DNA fragments of the ATK gene
 CC (T44527-37) are useful for analysis and diagnosis of XLA carriers and
 CC for gene therapy. Primers for amplifying the DNA fragments are given in
 CC T44528-59. The present sequence is encoded by T44529.
 XX
 SO Sequence 27 AA:

Query Match 54.9%; Score 28; DB 17; Length 27;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 APQEVKK 10
 :||:|:|:
 Db 12 spcclark 19

RESULT 14
 Y03800
 ID Y03800 standard; peptide; 28 AA.
 XX
 AC Y03800;
 XX
 DT 11-JUN-1999 (first entry)
 XX
 DE Murine LckBP1 peptide fragment P1.
 XX
 KW Lck binding protein; LckBP1; immunosuppressive; SH3 region; allergy;
 KW tyrosine kinase; immune disorder; autoimmune disease; allograft;
 KW xenograft rejection; cancer; murine.
 XX
 OS Mus sp.
 XX
 PN US5891673-A.
 XX
 PD 06-APR-1999.
 XX
 PF 01-OCT-1997; 97US-0942423.
 XX
 PR 23-DEC-1994; 94US-0362715.
 PR 01-OCT-1997; 97US-0942423.
 XX
 PA (SYNT) SYNTEX USA INC.
 XX
 PI Hashimoto Y; Takemoto Y;
 XX
 DR WPI; 1999-253858/21.
 XX
 PT Isolated 486 amino acid LckBP1 protein and fragments - useful for
 PT diagnosing tyrosine kinase modulated disorders and as
 PT immunosuppressive agents for treating allergies
 XX
 PS Example 11; Columns 23-24; 47pp; English.
 XX
 CC The invention relates to a murine Lck binding protein, LckBP1 having
 CC immunosuppressive activity. LckBP1 binds to and modulates Lck,
 CC particularly the SH3 region. The protein and its active fragments are
 CC useful for the diagnosis of tyrosine kinase modulated disorders e.g.
 CC immune disorders such as allergy, autoimmune disease, allograft/xenograft
 CC rejection and cancer. The present sequence represents a peptide fragment
 CC of murine LckBP1.
 XX
 SO Sequence 28 AA:

Query Match 54.9%; Score 28; DB 20; Length 28;
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 PVAPQEVKK 10
 :||:|:|:
 Db 15 paapaqlpkk 24

RESULT 15
 W07056
 ID W07056 standard; peptide; 9 AA.
 XX
 AC W07056;
 XX
 DT 21-JAN-1997 (first entry)
 XX
 DE Synthetic peptide used in GalNac-transferase activity SPA.
 XX
 KW SPA: scintillation proximity assay; antigen: bead coating; capture;
 KW antibody: N-acetyl galactosamine transferase; GalNac transferase;
 KW activity; enzyme; O-linked glycosylation.
 XX
 OS Synthetic.
 XX
 PN W09615258-A1.
 XX
 PD 23-MAY-1996.
 XX
 PF 08-NOV-1995; 95WO-US13483.
 XX
 PR 16-NOV-1994; 94US-0340283.
 XX
 PA (UPJO) UPJOHN CO.
 XX
 PI Elhammer AP;
 XX
 DR WPI; 1996-268220/27.
 XX
 PT Scintillation proximity assay for N-acetyl galactosaminyl activity
 PT - esp. for large scale screening of cpds. for their effect on enzyme
 PT activity
 XX
 PS Claim 14; Page 17; 29pp; English.
 XX
 CC W06985-W07180 are antigenic peptides derived from either the
 CC product of the human c-myc oncogene or the FLAG peptide (DYKDDK).
 CC The peptides are useful for coating beads used in a scintillation
 CC proximity assay for N-acetyl galactosamine (GalNac)-transferase (GNT)
 CC activity. The assay involves fewer steps than known assays and is
 CC quicker, producing excellent signal-to-noise ratios. The
 CC assay is capable of screening large numbers of cpds. for their
 CC ability to affect GNT activity and is thus useful for identifying
 CC inhibitors and promoters of glycosylation (in partic. O-linked
 CC glycosylation).
 XX
 SO Sequence 9 AA:

Query Match 52.9%; Score 27; DB 17; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2.1e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PVAPQ 6
 :||:|:
 Db 1 pvlptq 6

Search completed: February 13, 2001, 13:02:03
 Job time: 84 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:03:17 ; Search time 32.52 Seconds
(without alignments)
5.522 Million cell updates/sec

Title: US-09-372-036-31

Perfect score: 51

Sequence: 1 PVAPTOEVKK 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues 111283

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 30
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/3A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/3B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PTTUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2	US-08-456-670B-31
2	51	100.0	12	2	US-08-456-670B-30
3	51	100.0	21	1	US-08-127-499A-27
4	51	100.0	21	1	US-08-482-847-27
5	36	70.6	7	1	US-08-127-499A-28
6	36	70.6	7	1	US-08-482-847-28
7	32	62.7	9	2	US-08-456-670B-26
8	32	62.7	12	2	US-08-389-011-16
9	32	62.7	12	2	US-08-389-011-17
10	32	62.7	12	2	US-08-389-011-18
11	32	62.7	12	3	US-08-403-917A-16
12	32	62.7	12	3	US-08-403-917A-17
13	32	62.7	12	3	US-08-403-917A-18
14	32	62.7	20	2	US-08-456-670B-17
15	32	62.7	26	2	US-08-389-011-17
16	32	62.7	26	2	US-08-403-917A-7
17	28	54.9	11	5	5200183-12
18	28	54.9	28	2	US-08-942-423-9
19	27	52.9	9	2	US-08-340-283-81
20	27	52.9	12	1	US-08-354-685-2
21	27	52.9	12	2	US-08-389-011-15
22	27	52.9	12	3	US-08-403-917A-15
23	27	52.9	15	1	US-08-116-733-15
24	27	52.9	15	1	US-08-687-956A-6
25	27	52.9	17	1	US-08-553-703A-7
26	27	52.9	17	2	US-09-006-021-7
27	27	52.9	20	1	US-07-923-724-43
28	27	52.9	20	2	US-08-609-426A-43

29	27	52.9	21	1	US-08-127-499A-33	Sequence 33, Appl
30	27	52.9	21	1	US-08-482-847-33	Sequence 33, Appl
31	27	52.9	24	2	US-08-374-652C-32	Sequence 37, Appl
32	27	52.9	28	2	US-08-392-816-4	Sequence 4, Appl
33	27	52.9	30	2	US-08-459-568-84	Sequence 84, Appl
34	27	52.9	30	2	US-08-399-411-84	Sequence 84, Appl
35	27	52.9	30	3	US-08-516-859A-84	Sequence 19, Appl
36	26	51.0	12	2	US-08-389-011-19	Sequence 19, Appl
37	26	51.0	12	2	US-08-389-011-20	Sequence 20, Appl
38	26	51.0	12	2	US-08-389-011-21	Sequence 21, Appl
39	26	51.0	12	3	US-08-403-917A-19	Sequence 19, Appl
40	26	51.0	12	3	US-08-403-917A-20	Sequence 20, Appl
41	26	51.0	12	3	US-08-541-759B-3	Sequence 21, Appl
42	26	51.0	27	2	US-08-541-759B-3	Sequence 4, Appl
43	26	51.0	27	2	US-08-541-759B-4	Sequence 4, Appl
44	26	51.0	27	2	US-08-541-759B-5	Sequence 5, Appl
45	26	51.0	29	1	US-07-609-510B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-456-670B-31
Sequence 31, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, STEFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWILLER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: HUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-31

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTOEVKK 10
DB 1 PVAPTOEVKK 10

RESULT 2
US-08-456-670B-30
Sequence 30, Application US/08456670B
Patent No. 5932415.
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKEWELER, WINFRIED
APPLICANT: BUNGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-30

Query Match 100.0%; Score 51; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTOEVKK 10
DB 3 PVAPTOEVKK 12

RESULT 3
US-08-127-499A-27
Sequence 27, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-27

Query Match 100.0%; Score 51; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVAPTOEVKK 10
DB 5 PVAPTOEVKK 14

RESULT 4
US-08-482-847-27
Sequence 27, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-27

Query Match 100.0%; Score 51; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVAPTOEVKK 10
Db 5 PVAPTOEVKK 14

RESULT 5
US-08-127-499A-28
Sequence 28, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-28

Query Match 70.6%; Score 36; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PTOEVKK 10
Db 1 PTOEVKK 7

RESULT 6
US-08-482-847-28
Sequence 28, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-28

Query Match 70.6%; Score 36; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PROEVKK 10
| | | | |
DB 1 PROEVKK 7

RESULT 7
US-08-456-670B-26
Sequence 26, Application US/08456670B
Patent No. 5932415

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINKWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1694D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

TELEX: 64191

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
US-08-456-670B-26

Query Match 62.7%; Score 32; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPTO 6
| | | | |
DB 4 PVAPTO 9

RESULT 8

US-08-389-011-16
Sequence 16, Application US/08389011
Patent No. 5861257

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANNECHELEN, EUGENE; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROBUBBLE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.003-1-CON

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 12
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-16

Query Match 62.7%: Score 32; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PVAPTOEVKK 10
1 11:111
Db 3 PTPPTREPCK 12

RESULT 9
US-08-389-011-17
Sequence 17, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANNECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown

US-08-389-011-17

Query Match 62.7%: Score 32; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PVAPTOEVKK 10
1 11:111
Db 2 PTPPTREPCK 11

RESULT 10
US-08-389-011-18
Sequence 18, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANNECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown

Query Match 62.7%: Score 32; DB 2; Length 12;

Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
| | | | |
Db 1 PTPPTREPKK 10

RESULT 11
US-08-403-917A-16
; Sequence 16, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROBUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-403-917A-16

Query Match 62.7%; Score 32; DB 3; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
| | | | |
Db 3 PTPPTREPKK 12

RESULT 12
US-08-403-917A-17
; Sequence 17, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROBUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-403-917A-17

Query Match 62.7%; Score 32; DB 3; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
| | | | |
Db 2 PTPPTREPKK 11

RESULT 13
US-08-403-917A-18
; Sequence 18, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANMECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-18

Query Match 62.7%; Score 32; DB 3; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PVAPTOEVKK 10
1 11:111
Db 1 PTPPTREPK 10

RESULT 14
US-08-456-670B-17
Sequence 17, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXMEIER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HOFMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER

APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
TITLE OF INVENTION: LISTERIAS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Listeria monocytogenes
STRAIN: EGD
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-7
OTHER INFORMATION: /note= "SOME OR ALL xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14-20
OTHER INFORMATION: /note= "SOME OR ALL xaa AMINO ACIDS
OTHER INFORMATION: MAY BE ABSENT"
US-08-456-670B-17

Query Match 62.7%; Score 32; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVAPTO 6
1 11111
Db 8 PVAPTO 13

RESULT 15
US-08-389-011-7

; Sequence 7, Application US/08389011
; Patent No. 5861257
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGENE; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,011
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,916
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,003-1-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-08-389-011-7

Query Match 62.7%; Score 32; DB 2; Length 26;
Best Local Similarity 60.0%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PVAPTOEVKK 10
| | | | |
| | | | |
Db 11 PTPPTREPK 20

Search completed: February 13, 2001, 13:03:17
Job time: 157 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:02:42 ; Search time 35.7 Seconds

(Without alignments)
19.020 Million cell updates/sec

Title: US-09-372-036-31

Perfect score: 51

Sequence: 1 PVAPTOEVKK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 6242

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_66:***
2: PIR1:***
3: PIR2:***
4: PIR3:***
5: PIR4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	51.0	15	2	S68731
2	26	51.0	24	2	I50387
3	25	49.0	18	2	A28027
4	24	47.1	12	2	JU0356
5	24	47.1	18	2	A61220
6	24	47.1	20	2	A37111
7	24	47.1	21	2	PH1231
8	24	47.1	27	2	F36690
9	23	45.1	20	2	A61150
10	23	45.1	29	1	TNLJBR
11	22	43.1	16	2	PH1790
12	22	43.1	23	2	F61491
13	22	43.1	23	2	A49221
14	22	43.1	24	2	A56753
15	22	43.1	24	2	S23121
16	22	43.1	30	2	G71359
17	21	41.2	10	2	JP0072
18	21	41.2	13	2	PC1149
19	21	41.2	16	2	A24059
20	21	41.2	19	2	A33361
21	21	41.2	20	2	S72501
22	21	41.2	20	2	S13861
23	21	41.2	22	2	JC1488
24	21	41.2	24	2	PC2313
25	21	41.2	29	2	S03277
26	21	41.2	30	2	B60291
27	21	41.2	30	2	S28849
28	20	39.2	14	2	PH1806
29	20	39.2	15	2	PA0054

ALIGNMENTS

30	20	39.2	16	2	S38292	30K allergen - rye
31	20	39.2	20	2	S35970	ribosomal protein
32	20	39.2	21	2	A60225	pyruvate dehydrog
33	20	39.2	21	2	S35978	ribosomal protein
34	20	39.2	23	2	S35975	ribosomal protein
35	20	39.2	23	2	S35976	ribosomal protein
36	20	39.2	23	2	S37491	hypothetical prote
37	20	39.2	24	2	A56342	ada 3'-region alkB
38	20	39.2	24	2	B39433	2F3 domain - human
39	20	39.2	24	2	I39289	cytolytic enteroto
40	20	39.2	25	2	A30590	hypothetical prote
41	20	39.2	25	2	S13996	membrane alanyl am
42	20	39.2	25	2	A56864	alpha-amylase/lyp
43	20	39.2	29	2	C24536	carbon-monoxide de
44	19	37.3	9	2	PL0139	beta-glucosidase (
45	19	37.3	11	2	PQ0231	

RESULT 1
S68731
bleomycin-binding protein - Staphylococcus aureus (fragment)
C:Species: Staphylococcus aureus
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C:Accession: S68731
R: Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Na
FEBS Lett. 362, 80-84, 1995
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing St
al characterization.
A:Reference number: S68730; MUID:95212588
A:Accession: S68731
A:Molecule type: protein
A:Residues: 1-15 <SDS>
A:Experimental source: strain B-26
C:Keywords: antibiotic resistance

Query Match 51.0% Score 26; DB 2; Length 15;

Best Local Similarity 40.0% Pred. No. 75;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PVAPTOEVKK 10
DB 6 PALPVGDIKK 15

RESULT 2
I50387
c-myc protein - chicken (fragment)

C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I50387
R: Westaway, D.; Payne, G.; Varmus, H.E.

Proc. Natl. Acad. Sci. U.S.A. 81, 843-847, 1984
A:Title: Proviral deletions and oncogene base-substitutions in insertionally mutageni

A:Reference number: I50387; MUID:84144799
A:Accession: I50387

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-24 <MES>
A:Cross-references: GB:K01440; NID:g212357; PIDN:AAA48964.1; PID:g212358

Query Match 51.0% Score 26; DB 2; Length 24;

Best Local Similarity 40.0% Pred. No. 1.2e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
DB 2 PPAPSEDIVK 11

Query Match 47.1%; Score 24; DB 2; Length 27;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
| | : | : |
Db 14 PVLSTTELK 23

RESULT 9
A61150
2-oxoglutarate decarboxylase (EC 4.1.1.71) - *Euglena gracilis* (fragment)
C:Species: *Euglena gracilis*
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-Apr-1994
C:Accession: A61150
R:Shigeoka, S.; Nakano, Y.
Arch. Biochem. Biophys. 288, 22-28, 1991
A:Title: Characterization and molecular properties of 2-oxoglutarate decarboxylase from
A:Reference number: A61150; MUID:91378443
A:Accession: A61150
A:Molecule type: protein
A:Residues: 1-20 <SHIT>
C:Keywords: carbon-carbon lyase; carboxy-lyase; homotetramer; mitochondrion

Query Match 45.1%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 APPTQEVK 9
| | : | : |
Db 5 APVKDVK 11

RESULT 10
TNLJBR
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 02-Jul-1998
C:Accession: B31667
R:Amund, R.; Thayer, R.; Sriivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.
Virology 168, 79-89, 1989
A:Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)
A:Reference number: A94389; MUID:89085613
A:Accession: B31667
A:Molecule type: DNA
A:Residues: 1-29 <ANNA>
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: transcription regulation

Query Match 45.1%; Score 23; DB 1; Length 29;
Best Local Similarity 40.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
| | : | : |
Db 9 PPGPKESKK 18

RESULT 11
PH1790
T cell receptor alpha chain V region (clone 2PBL V alpha 24-6) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1790
R:Porcilli, S.; Fockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blo
A:Reference number: PH1754; MUID:93301585
A:Accession: PH1790
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <PQR>

Query Match 43.1%; Score 22; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PVAPT 5
| | : | : |
Db 8 PIRPT 12

RESULT 12
F61491
seed protein ws-6 - winged bean (fragment)
C:Species: *Psophocarpus tetragonolobus* (winged bean)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 03-May-1996
C:Accession: F61491
R:Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A:Title: Microsequence analysis of winged bean seed proteins electrophoretically
A:Reference number: A61491; MUID:89351606
A:Accession: F61491
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <HIR>
C:Superfamily: pathogenesis-related protein
C:Keywords: seed

Query Match 43.1%; Score 22; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVAP 4
| | : | : |
Db 12 PVAP 15

RESULT 13
A49221
14K aggregative adherence fimbriae I protein - *Escherichia coli* (fragment)
C:Species: *Escherichia coli*
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C:Accession: A49221
R:Nataro, J.P.; Yikang, D.; Girom, J.A.; Savarino, S.J.; Kotlary, M.H.; Hall, R.
Infect. Immun. 61, 1126-1131, 1993
A:Title: Aggregative adherence fimbria I expression in enteroadgregative *Escherichia*
A:Reference number: A49221; MUID:93162805
A:Contents: 17-2; serotype O3:H2
A:Accession: A49221
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <NAT>
A:Note: sequence extracted from NCBI backbone (NCBIP:125179)

Query Match 43.1%; Score 22; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 VAPTOEVK 9
| | : | : |
Db 10 VDSQXIK 17

RESULT 14

A56753
lysine-rich 18k protein - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-May-1997
C:Accession: A56753
R:Zhou, H.Y.; Ohnuma, Y.; Takita, H.; Fujisawa, R.; Mizuno, M.; Kuboki, Y.
Biochem. Biophys. Res. Commun. 186, 1288-1293, 1992
A:Title: Effects of a bone lysine-rich 18 kDa protein on osteoblast-like MC3T3-E1 cells.
A:Reference number: A56753; MUID:92378587
A:Accession: A56753
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-24 <ZHO>
A:Experimental source: tibia
A:Note: sequence extracted from NCBI backbone (NCBIP:111441)
C:Superfamily: pleiotrophin
C:Keywords: bone

Query Match 43.1%; Score 22; DB 2; Length 24;
Best Local Similarity 57.1%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PTOEVKK 10
I::IIII
DB 6 PEKKVKK 12

RESULT 15

S23121
1H-3-hydroxy-4-oxoquinoline oxygenase - Pseudomonas putida
C:Species: Pseudomonas putida
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S23121
R:Block, D.W.; Lings, F.
Biol. Chem. Hoppe-Seyler 373, 343-349, 1992
A:Title: Microbial metabolism of quinoline and related compounds. XIV. Purification and
rain 33/1.
A:Reference number: S23121; MUID:92384934
A:Accession: S23121
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-24 <BLO>

Query Match 43.1%; Score 22; DB 2; Length 24;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PVAPT 5
I::IIII
DB 19 PXAPT 23

Search completed: February 13, 2001, 13:02:42
Job time: 122 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:06:54 ; Search time 20.83 Seconds
(without alignments)
15.504 Million cell updates/sec

Title: US-09-372-036-31

Perfect score: 51

Sequence: 1 PVAPTOEVKK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1785

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	49.0	17	1 JHBP_PLAVG	P56675 platyrepia
2	22	43.1	30	1 Y161_TREPA	O83196 treponema p
3	21	41.2	15	1 UC08_MAIZE	P80614 zea mays (m
4	21	41.2	16	1 RL6_VIBPR	O56715 vibrio prot
5	21	41.2	30	1 LAST_PIG	P80171 sus scrofa
6	20	39.2	10	1 SPCR_RABIT	P36233 oryctolagus
7	20	39.2	13	1 ODDA_CANEA	P49823 canis famill
8	20	39.2	19	1 RL10_CITFR	P43448 citrobacter
9	20	39.2	20	1 RL10_PROVU	P51411 proteus vul
10	20	39.2	22	1 RL10_KLEPN	O47608 enterobacte
11	20	39.2	24	1 ALKE_SALTY	P37462 salmonella
12	20	39.2	24	1 DNAJ_SPRAG	P95694 streptococ
13	20	39.2	29	1 RP54_CLOKL	P38944 clostridium
14	20	39.2	9	1 DCML_PSECF	P19913 pseudomonas
15	19	37.3	13	1 UN02_PINPS	P81657 pinus pinas
16	19	37.3	21	1 APAL_ERYPB	P18647 erythrocebu
17	19	37.3	20	1 CXGT_CONVU	P17664 conus tulip
18	19	37.3	22	1 ODPX_BOVIN	P22439 bos taurus
19	19	37.3	24	1 KPRK_CLOPA	P80917 alcastridium
20	19	37.3	25	1 ACP_ALCEA	P80382 thecruus agu
21	19	37.3	25	1 RS20_THETH	O60829 mus musculu
22	19	37.3	27	1 IPPD_MOUSE	O60829 mus musculu
23	19	37.3	27	1 L52_ADRC07	P19371 desulfovibr
24	19	37.3	29	1 IPVR_DRSVH	P12312 human immun
25	19	37.3	30	1 TAT_HV12H	P12312 human immun
26	19	37.3	30	1 TAT_HV12H	P12312 human immun
27	18	35.3	19	1 ITBA_PERVAM	P19966 periplaneta
28	18	35.3	19	1 TCBI_TRLIO	P80070 trichoderma
29	18	35.3	20	1 ACPH_BOVIN	P80227 bos taurus
30	18	35.3	21	1 GYRA_STRSH	P50071 streptomyc
31	18	35.3	23	1 TBP2_PIC	P24853 sus scrofa
32	18	35.3	25	1 DNAB_MYCA	P71500 mycoblasma
33	18	35.3	28	1 ORND_PLAOR	P25513 placobdella

34	18	35.3	29	1 PSAF_SYNP6	P31083 synechococc
35	18	35.3	29	1 TAT_HV123	P12510 human immun
36	17	33.3	12	1 TM2A_METMA	P80652 methanosarc
37	17	33.3	14	1 UC15_MAIZE	P80621 zea mays (m
38	17	33.3	15	1 ESTJ_MANSE	P19985 manduca sex
39	17	33.3	17	1 A45K_MYCBO	P80069 mycobacteri
40	17	33.3	17	1 TRP2_LEUMA	P81733 leucophaea
41	17	33.3	19	1 ALL7_OLEEU	P81430 olea europa
42	17	33.3	19	1 COOT_SARBU	O09148 sarcophaga
43	17	33.3	20	1 CAPA_ACIRA	P81422 actinobact
44	17	33.3	20	1 COXF_ONCMY	P80329 oncothychnu
45	17	33.3	20	1 FRHA_METBA	P80469 methanosarc

ALIGNMENTS

RESULT 1	JHBP_PLAVG	STANDARD:	PRT:	17 AA.
ID	JHBP_PLAVG			
AC	P56675;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	JUVENILE HORMONE-BINDING PROTEIN (FRAGMENT).			
GN	JHBP.			
OS	Platyrepia virginialis (Ranchman's tiger moth).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pserygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylaria;			
OC	Noctuidae; Arctiidae; Platyrepia.			
RN	[1]			
RP	SEQUENCE.			
RA	Prestwich G.D., Atkinson J.K.;			
RT	"Rapid purification and N-terminal amino acid sequence of a			
RT	photoaffinity-labeled juvenile hormone binding protein from an arctiid			
RT	moth larva, Platyrepia virginialis.";			
RL	Insect Biochem. 20:801-807(1990).			
CC	-I- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING HYDROLYZED BY			
CC	GENERAL ESTERASES BY COMBINING WITH IT SPECIFICALLY.			
CC	-I- SUBCELLULAR LOCATION: SECRETED.			
FT	NON_TER			
FT	SEQUENCE			
FT	17 AA: 1880 MW: B1205F097732DA8A CRC64:			
Query Match	Best Local Similarity	49.0%;	Score 25;	DB 1; Length 17;
Matches	4; Conservative	2; Mismatches	0; Indels	0; Gaps
QY	5 TOEVKK 10			
Db	9 TQDIKK 14			
RESULT 2	Y161_TREPA	STANDARD:	PRT:	30 AA.
ID	Y161_TREPA			
AC	O83196;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	HYPOPHARYNGEAL PROTEIN TP0161.			
GN	TP0161.			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetales; Spirochaetaceae; Treponema.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-NICHOLS;			
RX	MEDLINE=98332770; Pubmed=9665876;			
RA	Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,			
RA	Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,			
RA	McDonald L., Arltach P., Bowman C., Cotton M.D., Fujii C., Garland S.,			

RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: A601200; AAC65153.1; -
 CC DR TIGR: TP0161; -
 KW Hypothetical protein.
 SO SEQUENCE 30 AA; 3259 MW; 4B9A413A5498D15F CRC64;

Query Match 43.1%; Score 22; DB 1; Length 30;
 Best Local Similarity 50.0%; Pred. No. 4; le+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

OY 1 PVAP--TOEVKK 10
 1:111111
 DB 8 PLRPGKTOESEK 19

RESULT 3
 UC08_MAIZE STANDARD; PRT; 15 AA.
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-COLEOPTILE;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huët J.-C.,
 RA Perollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996)
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 38.8 KDA.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 CC DR MAIZE-2DPAGE: P80614; COLEOPTILE.
 CC DR MAIZEDB: 123934; -
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6A4DDE8D CRC64;

Query Match 41.2%; Score 21; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 3; le+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTOE 7
 111111
 DB 9 PVPVGH 15

RESULT 4
 RL6_VIBPR STANDARD; PRT; 16 AA.
 AC 056715;

DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L6 (FRAGMENT).
 GN RPLP.
 OS Vibrio proteolyticus (Aeromonas proteolytica).
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15338;
 RX MEDLINE-97149305; PubMed-8996113;
 RA Settequist R.A., Smith G.K., Oakley T.H., Lee Y.H., Fox G.E.;
 RT "Sequence, overproduction and purification of Vibrio proteolyticus
 RT ribosomal protein L18 for in vitro and in vivo studies.";
 RL Gene 183:237-242(1996).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
 CC LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE
 CC PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U38943; AAB41328.1; -
 CC DR INTERPRO: IPR002358; -
 DR PROSITE: PS00525; RIBOSOMAL_L6_1; PARTIAL.
 KW Ribosomal protein; rRNA-binding.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1935 MW; ABC19078D5F581B6C CRC64;

Query Match 41.2%; Score 21; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 3; le+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 TOEVKK 10
 1:111111
 DB 10 TKRAKK 15

RESULT 5
 LAS1_PIG STANDARD; PRT; 30 AA.
 AC P80171;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE LIM AND SH3 PROTEIN 1 (LASP-1) (CYSTEINE-RICH PEPTIDE ZF-1)
 DE (FRAGMENT).
 GN Laspl.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-INTESTINE;
 RX MEDLINE-93145972; PubMed-8425549;
 RA Sillard R., Joernvall H., Carlqvist M., Mutt V.;
 RT "Chemical assay for cyst(e)ine-rich peptides detects a novel
 RT intestinal peptide ZF-1, homologous to a single zinc-finger motif.";
 RL Eur. J. Biochem. 211:377-380(1993).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE-96438771; PubMed-8841116;
 RA Hammarstrom A., Berndt K.D., Sillard R., Adernann K., Otting G.;
 RT "Solution structure of a naturally-occurring zinc-peptide complex
 RT demonstrates that the N-terminal zinc-binding module of the Laspl-1
 RT LIM domain is an independent folding unit.";

RL Biochemistry 35:12723-12732(1996).
 CC -1- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC IONS.
 DR PIR: S28849; S28849.
 DR PDB: 1ZFO: 08-NOV-96.
 DR INTERPRO: IPR001781; .
 DR PRAM: PR00412; LIM; 1.
 DR PROSITE: PS00478; LIM_DOMAIN_1; PARTIAL.
 DR PROSITE: PS50023; LIM_DOMAIN_2; 1.
 KM LIM motif: Metal-binding; zinc; Acetylation; 3D-structure.
 FT MOD_RES 1 1
 FT DOMAIN 5 >30 ACETYLATION.
 FT NON_TER 30 30 LIM.
 FT SEQUENCE 30 AA; 3517 MW; 042AB8FBE2314986 CRC64;
 SQ

Query Match 41.2%; Score 21; DB 1; Length 30;
 Best Local Similarity 57.18; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VAPTOEV 8
 DB 12 VYPTKV 18

RESULT 6
 ID SPRC_RABIT STANDARD; PRT; 10 AA.
 AC P36233;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SPARC (SECRETED PROTEIN ACIDIC AND RICH IN CYSTEINE) (OSTEOCONNECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40) (FRAGMENT).
 GN SPARC.
 OS Eukaryotes: Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Leporidae; Oryctolagus.
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-CARTILAGE.
 RX MEDLINE-94176562; Pubmed-8130279;
 RA Chandrasekhar S., Harvey A.K., Johnson M.G., Becker G.W.;
 RT "Osteonectin/SPARC is a product of articular chondrocytes/cartilage and is regulated by cytokines and growth factors.";
 RL Biochim. Biophys. Acta 1221:7-14(1994).
 CC -1- FUNCTION: APPEARS TO REGULATE CELL GROWTH THROUGH INTERACTIONS WITH THE EXTRACELLULAR MATRIX AND CYTOKINES. BINDS CALCITONIN AND COPPER. SEVERAL TYPES OF COLLAGEN, ALBUMIN, THROMBOSPONDIN, PDGF AND CELL MEMBRANES. THERE ARE TWO CALCIUM BINDING SITES; A ACIDIC DOMAIN THAT BINDS 5 TO 8 CA++ WITH A LOW AFFINITY AND A EF-HAND LOOP THAT BINDS A CA++ ION WITH A HIGH AFFINITY.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN TISSUES UNDERGOING MORPHOGENESIS, REMODELING AND WOUND REPAIR.
 CC -1- INDUCTION: BY GROWTH FACTORS SUCH AS TGF-BETA, PDGF, IGF-1.
 CC -1- SIMILARITY: CONTAINS AN OSTEOCONNECTIN-LIKE DOMAIN.
 DR PIR: S42762; S42762.
 DR INTERPRO: IPR001999; .
 DR INTERPRO: IPR002048; .
 DR PROSITE: PS00018; EF_HAND; PARTIAL.
 DR PROSITE: PS00612; OSTEOCONNECTIN_1; PARTIAL.
 DR PROSITE: PS00613; OSTEOCONNECTIN_2; PARTIAL.
 KM Extracellular matrix; Basement membrane; Glycoprotein;
 KW Calcium-binding; Copper.
 FT NON_TER 10 10
 FT SEQUENCE 10 AA; 1097 MW; DB5AB2672DD806C6 CRC64;
 SQ

Query Match 39.2%; Score 20; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 APTOE 7

Db 1 APOOE 5
 II II
 RESULT 7
 ID ODP_A_CANFA STANDARD; PRT; 13 AA.
 AC P49823;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT, SOMATIC FORM (EC 1.2.4.1) (PDH-E1 TYPE I) (FRAGMENT).
 GN PDH1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEART;
 RX MEDLINE-98163340; Pubmed-9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
 RT Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPAMIDE DEHYDROGENASE (E3).
 CC -1- CATALYTIC ACTIVITY: PYRUVATE + LIPAMIDE -> S-ACETYL-DIHYDRO-LIPOAMIDE + CO(2).
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
 CC -1- ENZYME REGULATION: E1 ACTIVITY IS REGULATED BY PHOSPHORYLATION (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVATION) OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 DR HSC-2DPAGE; P49823; DOG.
 KM Mitochondrion; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
 FT NON_TER 13 13
 FT SEQUENCE 13 AA; 1510 MW; C97EEBP844085B19 CRC64;
 SQ

Query Match 39.2%; Score 20; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 4.1e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 TOEVK 10
 DB 5 TFEIK 10

RESULT 8
 ID RL10_CITFR STANDARD; PRT; 19 AA.
 AC P43448;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L10 (FRAGMENT).
 GN RLJ.
 OS Citrobacter freundli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Citrobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-771;
 RA Zhyvoloup A.N.;
 RL Submitted (MIG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X74448; CAA52459.1; -
DR INTERPRO: IPR002363; -
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein.
FT INIT_MET 0 0 BY SIMILARITY.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2026 MW; E20A02CD7851DB16 CRC64;

Query Match 39.2%; Score 20; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 VAPTOEVKK 10
|| ||
Db 11 VAEVSEYAK 19

RESULT 9
ID R10_PROVU STANDARD; PRT; 20 AA.
AC P51411;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L10 (FRAGMENT).
GN RPLJ.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE FROM N.A.
RA Zhyvoloup A.N.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X74446; CAA52457.1; -
DR INTERPRO: IPR002363; -
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein.
FT INIT_MET 0 0 BY SIMILARITY.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2083 MW; 76520A02CD7851DB CRC64;

Query Match 39.2%; Score 20; DB 1; Length 20;
Best Local Similarity 55.6%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 VAPTOEVKK 10
|| ||
Db 11 VAEVSEYAK 19

RESULT 10
ID R10_KLEPN STANDARD; PRT; 22 AA.
DR INTERPRO: IPR002363; -
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.

AC P41190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L10 (FRAGMENT).
GN RPLJ.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.

CC EMBL: X74445; CAA52456.1; -
DR PIR: S35975; S35975.
DR PIR: S35976; S35976.
DR INTERPRO: IPR002363; -
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein.
FT INIT_MET 0 0 BY SIMILARITY.
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2268 MW; 113D96520A02CD78 CRC64;

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X74445; CAA52456.1; -
DR PIR: S35975; S35975.
DR PIR: S35976; S35976.
DR INTERPRO: IPR002363; -
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein.
FT INIT_MET 0 0 BY SIMILARITY.
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2268 MW; 113D96520A02CD78 CRC64;

Query Match 39.2%; Score 20; DB 1; Length 22;
Best Local Similarity 55.6%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 VAPTOEVKK 10
|| ||
Db 11 VAEVSEYAK 19

RESULT 11
ID R10_ENTCL STANDARD; PRT; 23 AA.
AC Q47608;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L10 (FRAGMENT).
GN RPLJ.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.

CC EMBL: X74444; CAA52455.1; -
DR INTERPRO: IPR002363; -
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X74444; CAA52455.1; -
DR INTERPRO: IPR002363; -
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.

KW Ribosomal protein.
FT INIT_MET 0 BY SIMILARITY.
RA NON_TER 23
SQ SEQUENCE 23 AA; 2355 MW; 39413D96520A02CD CRC64;

Query Match
Best Local Similarity 39.2%; Score 20; DB 1; Length 23;
Pred. No. 7.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 VAPTOEVK 10
| | | |
DB 11 VAEVSEYAK 19

RESULT 12
ALKB_SALTY STANDARD; PRT; 24 AA.
AC P37462;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ALKYLATED DNA REPAIR PROTEIN ALKB (FRAGMENT).
GN ALKB.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91267928; PubMed-1904855;
RT Hakura A., Morimoto K., Sofuni T., Nohmi T.;
RT Cloning and characterization of the Salmonella typhimurium ada gene,
RT which encodes O6-methylguanine-DNA methyltransferase.";
RL J. Bacteriol. 173:3663-3672(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE REPAIR OF ALKYLATED DNA.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: D90221; NOT_ANNOTATED_CDS.
CC PIR: B39433; B39433.
CC STYGENE: SGI0006; ALKB.
CC DNA repair.
CC NON_TER 24
FT SEQUENCE 24 AA; 2780 MW; CBB948C28FF908F3 CRC64;

Query Match
Best Local Similarity 39.2%; Score 20; DB 1; Length 24;
Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PVAPTQEV 8
| | | | |
DB 14 PLAPGRVY 21

RESULT 13
DNA_STRAG STANDARD; PRT; 24 AA.
AC P95694;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CHAPERONE PROTEIN DNAJ (FRAGMENT).
GN DNAJ.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus;

RN [1]
RP SEQUENCE FROM N.A.
RA Rioux C.R., Marlin D., Brodeur B.R.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INTERACTS WITH DNAK, TO DISASSEMBLE A PROTEIN COMPLEX
CC AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY
CC WITH GREP, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).
CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE DNAJ FAMILY.
CC -1- SIMILARITY: BELONGS TO THE DNAJ FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: U72719; AAB39220.1; -.
CC INTERPRO: IPR001305; -.
CC INTERPRO: IPR001623; -.
CC DR PROSITE: PS00636; DNAJ_1; PARTIAL.
CC DR PROSITE: PS50076; DNAJ_2; PARTIAL.
CC DR PROSITE: PS00637; DNAJ_CXXCXXG; PARTIAL.
CC FT Chapterone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
FT DOMAIN 3 >24 J-DOMAIN.
FT NON_TER 24
FT SEQUENCE 24 AA; 2760 MW; 342AE656E00913FC CRC64;

Query Match
Best Local Similarity 39.2%; Score 20; DB 1; Length 24;
Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 APTQEVK 10
| | | | |
DB 16 ASDDEIRK 23

RESULT 14
RP34_CLOKL STANDARD; PRT; 29 AA.
AC RP3444;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE RNA POLYMERASE SIGMA-54 FACTOR (FRAGMENT).
GN RPON OR SIGL.
OS Clostridium kluyveri.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-DSM 555;
RX MEDLINE-96146540; PubMed-8550525;
RA Soehling B., Gottschalk G.;
RT "Molecular analysis of the anaerobic succinate degradation pathway in
RT Clostridium kluyveri.";
RL J. Bacteriol. 178:871-880(1996).
CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC THEN IS RELEASED.
CC -1- SIMILARITY: BELONGS TO THE SIGMA-54 FACTOR FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: L21902; AAA92349.1; -
 DR INTERPRO: IPR000394; -
 DR PROSITE: PS00717; SIGMAS4_1; PARTIAL.
 DR PROSITE: PS00718; SIGMAS4_2; PARTIAL.
 DR PROSITE: PS50044; SIGMAS4_3; PARTIAL.
 KM Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
 KW DNA-binding.
 FT NON_TER 29
 SQ SEQUENCE 29 AA: 3413 MW: 7CD3A1E298AFFFA CRC64;

Query Match 39.2%; Score 20; DB 1; Length 29;
 Best Local Similarity 50.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 VAPTOEVK 9
 : | | | | :
 Db 13 LAMTOEMQ 20

RESULT 15
 DCML_PSECF STANDARD; PRT; 9 AA.
 ID DCML_PSECF
 AC P19913:
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
 OS Pseudomonas carboxydoflava.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
 OC Hydrogenophaga.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-90055678; PubMed-2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydoflagic bacteria";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
 CC ACCEPTOR.
 CC -1- COFACTOR: MOLYBDENUM.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: PL0139; PL0139.
 KW Oxidoreductase; Molybdenum.
 FT VARIANT 2 2
 FT NON_TER 9 9
 FT SEQUENCE 9 AA: 974 MW: 022ADAB6C2D76DD4 CRC64;

Query Match 37.3%; Score 19; DB 1; Length 9;
 Best Local Similarity 42.9%; Pred. No. 8.9e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 APVQDAE 9
 | | | :
 Db 3 APVQDAE 9

Search completed: February 13, 2001, 13:06:54
 Job time: 286 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 13:06:30 ; Search time 58.16 Seconds
(without alignments)
20.153 Million cell updates/sec

Title: US-09-372-036-31
Perfect score: 51
Sequence: 1 PVAPTOEVKK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 10868

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	56.9	29	12 091011	091q11 human immun
2	29	56.9	29	12 091010	091q10 human immun
3	26	51.0	23	11 063334	063334 rattus norv
4	26	51.0	23	12 0908P0	0908P0 australian
5	26	51.0	24	12 085618	085618 avian leuko
6	25	49.0	22	1 090W19	090W19 methanospir
7	24	47.1	17	5 09TWR3	09TWR3 trypanosoma
8	24	47.1	21	10 042417	042417 triticum ae
9	24	47.1	21	10 042501	042501 triticum ae
10	24	47.1	21	10 09S7S6	09S7S6 triticum ae
11	24	47.1	25	13 09PSB2	09PSB2 xenopus bor
12	24	47.1	27	12 0911S7	0911S7 hepatitis c
13	24	47.1	30	4 09P1D6	09P1D6 homo sapien
14	23	45.1	14	4 09UC70	09UC70 homo sapien
15	23	45.1	19	2 09RBV1	09RBV1 pseudomonas
16	23	45.1	20	5 09TWM8	09TWM8 leptinotars
17	23	45.1	21	10 0415S9	0415S9 triticum ae
18	23	45.1	21	10 041564	041564 triticum ae
19	23	45.1	24	11 09WVE6	09WVE6 mus musculu

20	23	45.1	25	6 09TRW8	09trw8 trichosurus
21	23	45.1	29	12 091QJ9	091qj9 human immun
22	23	45.1	29	12 091QJ7	091qj7 human immun
23	23	45.1	29	12 091QJ6	091qj6 human immun
24	23	45.1	29	12 091QJ5	091qj5 human immun
25	23	45.1	29	12 091QJ4	091qj4 human immun
26	23	45.1	29	12 091QJ3	091qj3 human immun
27	23	45.1	29	12 091QJ2	091qj2 human immun
28	23	45.1	29	12 091QJ0	091qj0 human immun
29	23	45.1	29	12 091QJ9	091qj9 human immun
30	23	45.1	29	12 091QJ8	091qj8 human immun
31	23	45.1	29	12 091QJ7	091qj7 human immun
32	23	45.1	29	12 091QJ6	091qj6 human immun
33	23	45.1	29	12 091QJ5	091qj5 human immun
34	23	45.1	29	12 091QJ3	091qj3 human immun
35	23	45.1	29	12 091QJ9	091qj9 human immun
36	23	45.1	30	2 09L8J9	09l8j9 enterobacte
37	23	45.1	30	2 09L8J9	09l8j9 enterobacte
38	23	45.1	30	2 09L8J9	09l8j9 enterobacte
39	22	43.1	11	5 09V7K6	09v7k6 klebsiella
40	22	43.1	13	4 09UCU2	09ucu2 homo sapien
41	22	43.1	16	4 016033	016033 homo sapien
42	22	43.1	17	4 09UCG6	09ucg6 homo sapien
43	22	43.1	17	6 09TR21	09tr21 sus scrofa
44	22	43.1	19	4 09UCN8	09ucn8 homo sapien
45	22	43.1	23	2 09R5D1	09r5d1 escherichia

ALIGNMENTS

RESULT 1					
091QJ1					
ID 091QJ1	PRELIMINARY:	PRT:	29 AA.		
AC 091QJ1:					
DT 01-OCT-2000 (TREMBlrel. 15, Created)					
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)					
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)					
DE TAT PROTEIN (FRAGMENT).					
GN TAT.					
OS Human immunodeficiency virus type 1.					
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.					
OX NCBI_Taxid=11676;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN-PATIENT 17;					
RA Yamada T., Iwamoto A.;					
RT "Comparison of proviral accessory genes between long-term					
RT nonprogressors and progressors of human immunodeficiency virus type 1					
RT infection."					
RL Arch. Virol. 145:1021-1027(2000).					
DR EMBL; AB034453; BAA93910.1; -.					
FT NON_TER	1				
FT SEQUENCE	29 AA;	3013 MW;	83CCFF3D51DA7255 CRC64;		
Query Match	56.9%	Score 29;	DB 12;	Length 29;	
Best Local Similarity	50.0%	Pred. No. 76;			
Matches 5;	Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;
Db	1 PVAPTOEVKK 10				
	1 11: 11				
RESULT 2					
091QJ0					
ID 091QJ0	PRELIMINARY:	PRT:	29 AA.		
AC 091QJ0:					
DT 01-OCT-2000 (TREMBlrel. 15, Created)					
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)					
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)					
DE TAT PROTEIN (FRAGMENT).					

GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirda; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT 17;
 RA Yamada T., Iwamoto A.;
 RT "Comparison of proviral accessory genes between long-term
 RT nonprogressors and progressors of human immunodeficiency virus type 1
 RT infection.";
 RL Arch. Virol. 145:1021-1027(2000).
 DR EMBL: AB034454; BAA93911.1; -.
 FT NON_TER
 SQ SEQUENCE 29 AA; 3085 MW; 83CF9F3D51DA7255 CRC64;

Query Match 56.9%; Score 29; DB 12; Length 29;
 Best Local Similarity 50.0%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
 | | | | |
 DB 9 PPGPTESKKK 18

RESULT 3
 ID 063334 PRELIMINARY; PRT; 23 AA.
 AC 063334;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
 DE ALPINA-2-MACROGLOBULIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR;
 RX MEDLINE=85207604; PubMed=2581948;
 RA Northmann W., Heisig M., Kunz D., Heinrich P.C.;
 RT "Molecular cloning of cDNA sequences for rat alpha 2-macroglobulin and
 RT measurement of its transcription during experimental inflammation.";
 RL J. Biol. Chem. 260:6200-6205(1985).
 DR EMBL: M84369; AAA1594.1; -.
 DR INTERPRO: IPR001599; -.
 DR PRAM: PF00207; AZM; 1.
 FT NON_TER
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2526 MW; E2D721FB1B223876 CRC64;

Query Match 51.0%; Score 26; DB 11; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 APTOE 7
 | | | | |
 DB 19 APTOE 23

RESULT 4
 ID 090SP0 PRELIMINARY; PRT; 23 AA.
 AC 090SP0;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
 DE L PROTEIN (FRAGMENT).
 CN L.
 OS Australian bat lyssavirus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 OX NCBI_TaxID=90961;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INSECTIVOROUS ISOLATE;
 RA Gould A.R., Kattenbelt J.A., Hyatt A.D., Gumley S.G., Lunt R.A.;
 RT "Characterisation of a variant of Australian Bat Lyssavirus isolated
 RT from an insectivorous bat and comparison to virus isolates from
 RT Pteropid bats.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF081020; AAD47900.1; -.
 FT NON_TER
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2599 MW; 7B584A2225E76530 CRC64;

Query Match 51.0%; Score 26; DB 12; Length 23;
 Best Local Similarity 55.6%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTOEVK 9
 | | | | |
 DB 14 PVEPEPELK 22

RESULT 5
 ID 085618 PRELIMINARY; PRT; 24 AA.
 AC 085618;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE RAV-2 PROVIRAL DNA, C-MYC (AA 44-67), ALLELE L13 (FRAGMENT).
 OS Avian leukosis virus.
 OC Viruses; Retrovirda; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11864;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84144799; PubMed=6322173;
 RA Westaway D., Payne G., Varmus H.E.;
 RT "Proviral deletions and oncogene base-substitutions in insertionally
 RT mutagenized c-myc alleles may contribute to the progression of avian
 RT bursa tumors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:843-847(1984).
 DR EMBL: K01439; AAA51600.1; -.
 FT NON_TER
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2679 MW; 93F59F2D3B24E527 CRC64;

Query Match 51.0%; Score 26; DB 12; Length 24;
 Best Local Similarity 40.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 PVAPTOEVKK 10
 | | | | |
 DB 2 PPAPSEDIMK 11

RESULT 6
 ID 090WT9 PRELIMINARY; PRT; 22 AA.
 AC 090WT9;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
 DE 5 KDA FLAGELLIN (FRAGMENT).
 OS Methanospirillum hungatei.
 OC Archaea; Euryarchaeota; Methanomicrobiales; Methanomicrobiaceae;
 OC Methanospirillum.
 OX NCBI_TaxID=2203;
 RN [1]
 RP SEQUENCE.

RA MEDLINE-95095917; PubMed-8002572;
RA Faguy D.M., Koval S.F., Jarrell K.F.;
RT "Physical characterization of the flagella and flagellins from
RT *Mechanospirillum hungatei*."
RL J. Bacteriol. 176:7491-7498(1994).
SQ SEQUENCE 22 AA; 2360 MW; 168505F2B4F79E5 CRC64;

Query Match 49.0%; Score 25; DB 1; Length 22;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAPTOEVK 9
: ||: ||
DB 8 LVPTKVK 15

RESULT 7
Q9TWK3 PRELIMINARY; PRT; 17 AA.
AC Q9TWK3:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HISTONE H1 (FRAGMENT).
OS Trypanosoma cruzi.
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE.
RA MEDLINE-94043510; PubMed-8227175;
RA Toro G.C., Galanti N., Hellman U., Wernstedt C.;
RT "Unambiguous identification of histone H1 in Trypanosoma cruzi."
RL J. Cell. Biochem. 52:431-439(1993).
SQ SEQUENCE 17 AA; 1820 MW; AD19BCC52D8ECCD5 CRC64;

Query Match 47.1%; Score 24; DB 5; Length 17;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 APTOEVK 10
: ||: ||
DB 5 APTKAVK 12

RESULT 8
Q42417 PRELIMINARY; PRT; 21 AA.
AC Q42417:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
GN HSP16.9-17LC3.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
OX NCBI_Taxid=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUSTANG;
RA Joshi C.P., Nguyen H.T.;
RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RL EMBL: L37070; AAAS1390.1; -;
DR EMBL: L37068; AAAS1388.1; -;
DR EMBL: L37069; AAAS1389.1; -;
KW Heat shock.
FT NON_TER 1 1
SQ SEQUENCE 21 AA; 2266 MW; 489524EDE9A0527F CRC64;

Query Match 47.1%; Score 24; DB 10; Length 21;

Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PTOEVK 10
: ||||
DB 5 PKAEVK 11

RESULT 9
Q42501 PRELIMINARY; PRT; 21 AA.
AC Q42501:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
GN HSP16.9-5LC1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
OX NCBI_Taxid=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUSTANG;
RA Joshi C.P., Nguyen H.T.;
RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RL EMBL: L37075; AAAS1395.1; -;
DR EMBL: L37067; AAAS1387.1; -;
KW Heat shock.
FT NON_TER 1 1
SQ SEQUENCE 21 AA; 2223 MW; 522524F029A0527F CRC64;

Query Match 47.1%; Score 24; DB 10; Length 21;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PTOEVK 10
: ||||
DB 5 PKAEVK 11

RESULT 10
Q9S7S6 PRELIMINARY; PRT; 21 AA.
AC Q9S7S6:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE HEAT SHOCK PROTEIN 16.9 (FRAGMENT).
GN HSP16.9-8LC3 OR HSP16.9-14LC1 OR HSP16.9-2LC2 OR HSP16.9-3LC1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
OX NCBI_Taxid=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MUSTANG;
RA Joshi C.P., Nguyen H.T.;
RT "Differential display mediated rapid cloning and sequencing of the 3' region of several members of a large multigene family."
RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RL EMBL: L37076; AAAS1396.1; -;
DR EMBL: L37066; AAAS1386.1; -;
DR EMBL: L37072; AAAS1392.1; -;
DR EMBL: L37073; AAAS1393.1; -;
KW Heat shock.
FT NON_TER 1 1
SQ SEQUENCE 21 AA; 2224 MW; 522524EDE9A0527F CRC64;

Query Match 47.1%; Score 24; DB 10; Length 21;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PTOEVKK 10
1 1111
Db 5 PRAEVKK 11

RESULT 11

O9PSB2 PRELIMINARY; PRT; 25 AA.
ID O9PSB2
AC O9PSB2
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, last annotation update)
DE TYROSINE KINASE (FRAGMENT).
OS Xenopus borealis (Kenyan clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95290092; PubMed=7772253;
RA Islam N., Guimond A., Sanchez A., Moss T.;
RT "An analysis of Xenopus tyrosine kinase genes and their expression in
early development.";
RL DNA Cell Biol. 13:719-729(1994).
SQ SEQUENCE 25 AA; 3069 MW; E439ACB2CB2D9E CRC64;

Query Match 47.1%; Score 24; DB 13; Length 25;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 APTQEVKK 10
1 1111
Db 5 APERIRKK 12

RESULT 12

O9IIS7 PRELIMINARY; PRT; 27 AA.
ID O9IIS7
AC O9IIS7
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
DE ENVELOPE PROTEIN (FRAGMENT).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberto S.-F.;
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the
histological outcome of liver transplantation.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221336; AAF77930.1; -
FT NON_TER 1 1
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 2708 MW; CB775D6A5B5284AE CRC64;

Query Match 47.1%; Score 24; DB 12; Length 27;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VAPTQEV 8
1 1111
Db 21 VAPSQRI 27

RESULT 13

O9PID6 PRELIMINARY; PRT; 30 AA.
ID O9PID6
AC O9PID6
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
DE PRO2386 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,
Liu M., He F.;
RT "Functional prediction of the coding sequences of 121 new genes
deduced by analysis of cDNA clones from human fetal liver.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF116700; AAF71120.1; -
FT NON_TER 1 1
SQ SEQUENCE 30 AA; 3095 MW; B867AC02CAE6054A CRC64;

Query Match 47.1%; Score 24; DB 4; Length 30;
Best Local Similarity 62.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PVAPTQEV 8
1 1111
Db 13 PAASTQSV 20

RESULT 14

O9UCTO PRELIMINARY; PRT; 14 AA.
ID O9UCTO
AC O9UCTO
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE BASIC PROLINE-RICH PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92082469; PubMed=1747107;
RA Ramasubbu N., Reddy M.S., Bergey E.J., Haraszthy G.G., Soni S.D.,
Levine M.J.;
RT "Large-scale purification and characterization of the major
phosphoproteins and mucins of human submandibular-sublingual saliva.";
RL Biochem. J. 280:341-352(1991).
SQ SEQUENCE 14 AA; 1435 MW; DC513E0923990A6D CRC64;

Query Match 45.1%; Score 23; DB 4; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PVAPTQ 6
1 1111
Db 5 PLAPQ 10

RESULT 15

O9RBV1 PRELIMINARY; PRT; 19 AA.
ID O9RBV1
AC O9RBV1
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE INTEGRASE (FRAGMENT).

OS Pseudomonas sp. R9;
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=101164;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R; TRANSPOSON-TETRACYCLINE RESISTANCE TETC;
 RX MEDLINE=20011227; PubMed=10543801;
 RA Schmechel E.L., Jones A.L.;
 RT "Distribution of tetracycline resistance genes and transposons among
 phytoplasm bacteria in Michigan apple orchards.";
 RL Appl. Environ. Microbiol. 65:4898-4907(1999).
 DR EMBL, AF157798; ADD7998.1;...
 FT NON_TER
 SQ SEQUENCE 19 AA; 2065 MW; 19EF26DDCA6290F0 CRC64;

Query Match 45.18; Score 23; DB 2; Length 19;
 Best Local Similarity 44.48; Pred. No. 7.3e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PVAPTOEVK 9
 | : | : | |
 Db 7 PLPPLRSVK 15

Search completed: February 13, 2001, 13:06:30
 Job time: 312 sec

This Page Blank (uspto)